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August 3, 2004, 09:32:25; Search time 57 Seconds (without alignments) 3316.215 Million cell updates/sec
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Compugen Ltd.
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GenCore version (c) 1993 - 2004
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Database

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	Description	Abb08420 Catalytic	Add06430 Variant T	0	Aay01541 Alpha(2-3	н	Adc21533 T. cruzi	Adc21529 T. cruzi	Adc21530 T. cruzi	Aay44454 T. cruzi	Aay44455 Modified	-	Aar42014 Protein w	Aar42015 Trans-sia	Aar42016 TCNA Tran	Aaw26541 Trypanoso	0		Abb80239 Synthetic	Aaw48868 Pasteurel	Aaw02207 Bacteroid	Aar47061 Bacteroid	Abu02167 S. pneumo	Abp81446 Streptoco		Aay34376 Porphorym
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ALIGNMENTS

Mycoplasma associated disease; cell proliferation; trans-sialidase; enzyme; atherosclerotic vascular disease; malignancy; sialic acid; antiatherosclerotic; antibacterial; antiviral; anti-HIV; cytostatic; vasotropic; ovarian carcinoma; breast cancer; prostate cancer; colon cancer; lung cancer; leukaemia; HIV; human immunodeficiency virus; chlamydia; PCR primer. Catalytic trans-sialidase unit of T. cruzi amino acid sequence. ABB08420 standard; protein; 669 AA. 03-JUL-2001; 2001WO-BR000083. 03-JUL-2000; 2000BR-00002989. (first entry) (HIGU/) HIGUCHI M D (SCHE/) SCHENKMAN S. Trypanosoma cruzi. Synthetic. WO200202050-A2. 01-JUL-2002 10-JAN-2002. ABB08420; ABB0842

Higuchi MDL, Schenkman S;

WPI; 2002-154675/20. N-PSDB; ABA98876.

Composition useful for treatment of mycoplasma infection and diseases associated with cell proliferation e.g. malignancy or with co-infection with another microbe, comprises agent inhibiting sialic acid-mediated attachment of mycoplasma.

Claim 6; Fig 26; 63pp; English.

The invention relates to a composition useful for treating or preventing mycoplasma infection in a subject suffering from a disorder characterised by increased cell proliferation or by co-infection with a second microbe, comprising an agent that prevents or inhibits sialic acid-mediated attachment of mycoplasma to the subject's cells. The activity of

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antibacterial, antiviral, mit. HIV, cuestatic and vasotropic. The compositions are useful to treat diseases associated with undesirable cell proliferation, such as atherosclerotic vascular disease and malignancy, by reducing or preventing mycoplasma infection. Examples of colon cancer, lung cancer and leukaemia. They are also useful to treat diseases associated with infection with other infections organisms co-courring with mycoplasma (and typically increasing the virulence of both pathogens), especially human immunodeficiency virus or chlamydia species. They can be used to treat such diseases in humans or other animals, and can be administered in conjunction with conventional agents e.g. antiplatelet or chemotherapeutic agents. The current sequence represents the catalytic trans-sialidase unit of T. cruzi amino acid sequence
   compositions of the invention may
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Mycoplasma infection; cell proliferation; co-infection; parasite; respiratory epithelium; urogenital tract; infection; AIDS; autoimmune; sialic acid-mediated attachment; antibiotic; neuraminidase; trans-sialidase; neoplastic cell; apoptosis; atherosclerctic vascular disease; malignant disease; tumour; human immunodeficiency virus; HIV; Chlamydia; antibacterial; antiarteriosclerctic; cytostatic; anti-HIV; enzyme.

Trypanosoma cruzi.

Synthetic.

US2003124109-A1.

03-JUL-2003

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T. cruzi trans-sialidase enzyme.

(first entry)

01-JAN-2004

ADD06430;

NVDGVMVAIADARYETSNDNSLIDTVAKYSVDDGETWETQIAIKNSRASSVSRVVDPTVI 120 61 NVDGVMVAIADARYETSNDNSLIDTVAKYSVDDGETWETQIAIKNSRASSVSRVVDPTVI 120 VKGNKLYVLVGSYNSSRSYWTSHGDARDWDILLAVGEVTKSTAGGKITASIKWGSPVSLK 180 1 MGSSHHHHHHSSGLVPRGSHMAPGSSRVELFKRQSSKVPFEKGGKVTERVVHSFRLPALV **EFFPAEMEGMHTNQFLGGAGVALVASNGNLVYPVQVTNKKKQVFSKIFYSEDEGKTWKFG** EFFPAEMEGMHTNQFLGGAGVAIVASNGNLVYPVQVTNKKKQVFSKIFYSEDEGKTWKFG **EGRSDFGCSEPVALEWEGKLIINTRVDYRRRLVYESSDMGNSWVEAVGTLSRVWGPSPKS** NQPGSQSSFTAVTIEGMRVMLFTHPLNFKGRWLRDRLNLWLTDNQRIYNVGQVSIGDENS AYSSVLYKDDKLYCLHEINSNEVYSLVFARLVGELRIIKSVLQSWKNWDSHLSSICTPAD ASSVLYKDDKLYCLHEINSNEVYSLVFARLVGELRIIKSVLQSWKNWDSHLSSICTPAD PAASSSERGCGPAVTTVGLVGFLSHSATKTEWEDAYRCVNASTANAERVPNGLKFAGVGG Gaps GALWPVSQQGQNQRYHFANHAFTLVASVTIHEVPSVASPLLGASLDSSGGKKLLGLSYDE KHQWQPIYGSTPVTPTGSWEMGKRYHVVLTMANKIGSVYIDGEPLEGSGQTVVPDGRTPD ISHFYVGGYGRSDMPTISHVTVNNVLLYNRQLNAEEIRTLFLSQDLIGTEAHMGSSSGSS 0 Query Match 100.0%; Score 3517; DB 5; Length 669; Best Local Similarity 100.0%; Pred. No. 4.9e-290; Matches 669; Conservative 0; Mismatches 0; Indels 0; 0; Indels Sequence 669 AA; 61 361 481 (121 181 181 301 241 241 301 421 421 541 481 601

Use of an agent that prevents or inhibits Mycoplasma infection, for manufacturing a medicament for treating or preventing a disorder associated with increased cell proliferation, e.g. atherosclerotic

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ij

HIGUCHI M I

(HIGU/) (SCHE/)

Higuchi MDL, Schenkman

180 240 240 300 300 360

WPI; 2003-810968/76.

N-PSDB; ADD06429.

vascular disease or malignancy

03-JUL-2000; 2000BR-00002989. 03-JUL-2001; 2001BR-00002648. 03-JUL-2001; 2001WO-BR000083. 01-MAR-2002; 2002US-00086913

360 420 420 480 480 540 540 9 99 99 PAASSSERGCGPAVTTVGLVGFLSHSATKTEWEDAYRCVNASTANAERVPNGLKFAGVGG 699 699 ERSTPGSGC ERSTPGSGC 601 661 199

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Mycoplasma infection for manufacturing a medicament for treating a disorder associated with increased cell proliferation or a co-infection with mycoplasma and a second microbe. Mycoplasmas are parasites of the respiratory epithelium and ucrobe. Mycoplasmas are parasites of the respiratory epithelium and ucropental tract. Infections are typically asymptomatic but they seem to be co-factors in diseases such as AIDS and in sequelae after mycoplasma infections having an autoimmune basis. The agent prevents or inhibite sialic acid-mediated attachment of mycoplasma correct consisting of neuraminidase and/or trans-sialidase acitivity. The activity consisting of neuraminidase and/or trans-sialidase acitivity. The caryme is derived from a Trypanosoma cruzi microorganism, where the enzyme is a native or a recombinant enzyme. Results showed that trans-sialidase is effective as a drug in the treatment of neoplasma; removing mycoplasmas from the neoplastic cells leading to their apoptosis. The composition or the agent that prevents or inhibits mycoplasma infection is useful for manufacturing a medicament for treating or preventing a disorder associated with increased cell proliferation, e.g. charcoslerotic vascular disease or malignant disease (tumour), or a disease associated with increased cell proliferation, e.g. cuch as human immunodeficiency virus or a Chlamydia microbe. The sequence cuch as human immunodeficiency virus or a Chlamydia microbe. The sequence composition and a second microbe composition and a second microbe composition and a second microbe composition are a chlamydia microbe. The sequence composition is the variant T. cruzi trans-sialidase enzyme. The invention discloses the use of an agent that prevents or inhibits Query Match
100.0%; Score 3517; DB 7;
Best Local Similarity 100.0%; Pred, No. 4.9e-290;
Matches 669; Conservative 0; Mismatches 0; Claim 6; SEQ ID NO 2; 32pp; English. Sequence 669 AA;

MGSSHHHHHHSSGLVPRGSHMAPGSSRVELFKRQSSKVPFEKGGKVTERVVHSFRLPALV Gaps ö Indele

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RESULT 2 ADD06430

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Ą ADD06430 standard; protein; 669

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The present sequence represents Trypanosoma cruzi alpha(2-3) trans-
c sialidase. The protein is used in the method of the invention to produce
sialyl-oligosaccharides, particularly sialylactose, which are produced
by treating a dairy source such as a cheese processing waste strain with
c an alpha (2-3) trans-sialidase. The method can be used for producing
c sialyl-oligosaccharides, such as (2-3) sialyllactose for pharmaceutical
cuse. (2-3) sialyllactose has been shown to neutralise enterotoxins of
c various pathogenic microbes including B. coli, vibrio cholerae and
c Salmonella. It has also been shown that alpha(2-3) (2-3) sialyllactose
c (alpha-Neu5Ac-(2-3)-Gal-beta-(1-4)-Glc) interferes with colonisation of
thelicobacter pylori and thereby prevents or inhibits gastric and duodenal
c ulcers. (2-3) sialyllactose has additionally been proposed to inhibit
c immune complex formation by disrupting occupancy of the Pc carbohydrate
binding site on IgG and to be useful in treating arthritis
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                                                                                           Production of sialyl-oligosaccharides, particularly sialyl-lactose - by treating a dairy source such as a cheese processing waste stream with an
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llarity 99.2%; Pred. No. 2.3e-276;
Conservative 2; Mismatches 3;
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alpha (2-3) trans-sialidase.
WA,
Barker
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Pelletier M,
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                                     NVDGVMVAIADARYETSNDNSLIDTVAKYSVDDGETWETQIAIKNSRASSVSRVVDPTVI
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TSHGDARDWDILLAVGEVTKSTAGGKITASIKWGSPVSLKEFFPAEMEGMHTNQFLGGAG 181
                                                                                                                                                                                                                                                                                                                     GFLSHSATKTEWEDAYRCVNASTANAERVPNGLKFAGVGGGALWPVSQQGQNQRYHFANH 500
                                                                                                                                                                                                                                                                                                                                                  GFLSHSATKTEWEDAYRCVNASTANAERVPNGLKFAGVGGGALWPVSQQGQNQRYRFANH 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trans-sialidase, TS; neurotrophic peptide; interleukin-6; 
IL-6 secretion inducing peptide; neuron; glial cell; trophic support; 
ciliary neurotrophic factor; CNTF; leuksemia inhibitory factor; LIF; 
amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease; 
Huntington's disease; Chagas 'disease; peripheral neuropathy; palsy; 
multiple sclerosis; stroke; brain trauma; spinal cord trauma;
                                              VAIVASNGNLVYPVQVTNKKKQVFSKIFYSEDEGKTWKFGEGREDFGCSEPVALEWEGKL
                                                                   IINTRVDYRRRLVYESSDMGNSWVEAVGTLSRVWGPSPKSNQPGSQSSFTAVTIEGMRVM
                                                                                                                                                                                  LPTHPLNFKGRWLRDRLNLWLTDNQRIYNVGQVSIGDENSAYSSVLYKDDKLYCLHBINS
                                                                                                                                                                                                        NEVYSLVFARLVGELRIIKSVLQSWKNWDSHLSSICTPADPAASSSERGCGPAVTTVGLV
                                                                                                                                                                                                                                                                              AFTLVASVTIHEVPSVASPLLGASLDSSGGKKLLGLSYDEKHQWQPIYGSTPVTPTGSWE
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/note= "Signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC21501 standard; protein; 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peripheral nerve trauma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Production of sialyl-oligosaccharides, particularly sialyl-lactose - by treating a dairy source such as a cheese processing waste stream with an alpha (2-3) trans-sialidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                   Alpha(2-3)trans-sialidase; sialyl-oligosaccharide; sialyllactose; cheese processing waste strain; (2-3)sialyllactose; gastric ulcer; duodenal ulcer; arthritis; enterotoxin.
                                                                                                                                                                                                    Alpha(2-3) trans-sialidase sequence lacking amino acid repeats.
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Length 642;
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97.8%; Pred. No. 5.9e-269;
iive 6; Mismatches 8;
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                                                                                                  AAY01541 standard, protein;
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                                                                                                                                                                                                                                                                                                          Trypanosoma cruzi.
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les 626; Conserv
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Pereira
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                                                                                                               The invention relates to a T. cruzi trans-sialidase (TS) derived neurotrophic peptide appearing as ADC21513 or ADC21511 called C44 and C14, or its variant, and an interleukin-6 (IL-6) secretion inducing peptide appearing as ADC21531 called TR-1 (terminal repeat 1). Also included are a composition comprising the peptides and a fusion partner, a composition comprising the peptides and a fusion partner, a composition comprising the fusion protein and a physiological acceptable carrier, providing trophic support for neurons or gilal cells in a mammal (comprising administering a therapeutically effective amount of T. cruzi transcalministering at the fusion partner of mammal (comprising administering a caministering a therapeutically effective amount of T. cruzi transcalministering of IL-6 (interleukin-6) in a mammal comprising administering or an IL-6 inducing variant. The fusion partner comprises a mammalian neurorrophic factor which is ciliary neurotrophic factor (LIF). The peptides are useful in providing trophic support for neurons and glial cells in a mammal suffering a condition selected from: amyotrophic lateral sclerosis, Alzheimer's disease, Paxinson's disease, Chagae disease, chagae disease, peripheral neuropathy, palsies, multiple sclerosis, stroke, brain trauma, spinal cord trauma and peripheral nerve trauma, and in stimulating the secretion of IL-6. The present sequence represents trans-sialidase clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                      T. cruzi trans-sialidase derived neurotrophic and interleukin-6 secretion inducing peptides, useful in the treatment of neuronal degeneration caused for example by Chagas' disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVAIVASNGNLVYPVQVTNKKKQVFSKIFYSEDEGKTWKFGEGRSDFGCSEPVALEWEGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 MLFTHPLNFKGRWLRDRLNLWLTDNQRIYNVGQVSIGDENSAYSSVLYKDDKLYCHHEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSLIDIVAKYSVDDGETWETQIAIKNSRASSVSRVVDPTVIVKGNKLYVLVGSYNSSRSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                88.4%; Score 3110.5; DB 7; 93.8%; Pred. No. 1.9e-255; ive 18; Mismatches 20;
                                                                                          Disclosure; SEQ ID NO 2; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 93.8% see 595; Conservative
2003-786654/74.
            N-PSDB; ADC21500
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 666 AA;
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The invention relates to a T. cruzi trans-sialidase (TS) derived neurotrophic peptide appearing as ADC21513 or ADC21511 called C44 and neurotrophic peptide appearing as ADC21531 or ADC21511 called C44 and C14, or its variant, and an interleukin-6 (IL-6) secretion inducing peptide appearing as ADC21531 called TR-1 (terminal repeat 1). Also included are a composition comprising the peptides and a fusion partner, a composition comprising the fusion protein and a physiological acceptable carrier, providing trophic support for neurons or gilal cells in a mammal (comprising administering a therapeutically effective amount of T. cruzi transaluliase (TS) or a neurotrophic variant) and stimulating (M3) the secretion of IL-6 (interleukin-6) in a mammal comprising administering TS or an IL-6 inducing variant. The fusion partner comprises a mammalian neurotrophic factor which is ciliary neurotrophic factor (CNTF) or neurotrophic factor (LIF). The peptides are useful in providing trophic support for neurons and gilal cells in a mammal suffering a condition selected from: amyotrophic lateral sclerosis, Alzheimer's ginal cord trauma and peripheral nerve trauma, and in stimulating the secretion of IL-6. The present sequence represents trans-sialidase clone
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                                                ETGKRYHLVLTWANKIGSVYIDGELLEGSGGTVVPDGRTPDISHPVVGGYKRSDMPTISH
EMGKRYHVVLTMANKIGSVYIDGEPLEGSGOTVVPDGRTPDISHFYVGGYGRSDMPTISH
                                                                                                                                                                                  653
                                                                                                                                                                                                                                                                         999
                                                                                                                                                                                                                                       VIVNINVLLYNRQLNTEEIRTLFLSQDLIGTEAHM
                                                                                                                                                                                  VIVNNVLL YNROLNAEEIRTLFLSODLIGTEAHM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T. cruzi trans-sialidase, TS, clone 7F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC21533 standard; protein; 1162
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20-DEC-2000; 2000US-00745008

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125
                                                                       126 LYVLVGSYNSSRSYWTSHGDARDWDILLAVGEVTKSTAGGKITASIKWGSPVSLKEFFPA 185
                                                                                               120
                                                                                                                 245
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                                                                                                                                                     305
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                                                                                                                                                                                    QSSFTAVTIEGMRVMLFTHPLNFKGRWLRDRLNLWLTDNQRIYNVGQVSIGDENSAYSSV 365
                                                                                                                                                                                            LYKDDKLYCLHEINSNEVYSLVFARLVGELRIIKSVLOSWKNWDSHLSSICTPADPAASS 425
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                                   66 MVAIADARYETSNDNSLIDTVAKYSVDDGETWETQIAIKNSRASSVSRVVDPTVIVKGNK
                                              EMEGMHTNQFLGGAGVAIVASNGNLVYPVQVTNKKKQVFSKIFYSEDEGKTWKFGEGRSD
                                                                                                                       FGCSEPVALEWEGKLIINTRVDYRRRLVYESSDMGNSWVEAVGTLSRVWGPSPKSNQPGS
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                          426 SERGCGPAVTIVG----LVGFLSHSATKIEWEDAYRCVNASTANAERVPNGLKFAGVGGG
                                                                                                                                                                                                                                                                           357 PLRRQRVVVVPLSPRLVLLAFCRQRLPK-RMGGSYRCVNASTANAERVRNGLKFAGVGGG
                                                                                                                                                                                                                                                                                                           SHFYVGGYCRSDMPTISHVTVNNVLLYN-ROLNAEEIRTLFLSQDLIGTEAHMGSSSGSS
                                                                                                                                                                                                                                                                                               ALWPVSQQGQNQRYHFANHAFTLVASVTIHEVPSVASPLLGASLDSSGGKKLLGLSYDEK
                                                                                                                                                                                                                                                                                                                                  HOWOPIYGSTPVTPTGSWEMGKRYHVVLTMANKIGSVYIDGEPLEGSGQTVVPDGRTPDI
                                                                                                                                                                                                                                                                                                                                             10;
    Length 1162;
                     50; Indels
76.2%; Score 2681; DB 7;
86.5%; Pred. No. 1.7e-218;
ive 22; Mismatches 50;
                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           596 AHSTPST 602
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        Similarity
                 525;
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Query Match
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        Local
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Trans-sialidase; TS; neurotrophic peptide; interleukin-6; 
IL-6 secretion inducing peptide; neuron; glial cell; trophic support; 
ciliary neurotrophic factor; CNTF; leukaemia inhibitory factor; LIF; 
amyotrophic lateral sclerosis; Alzheimer's disease; Parkinson's disease; 
Huntington's disease; Chagas' disease; peripheral neuropathy; palsy; 
peripheral nerve trauma.
                                                                                                                                                                                                 cruzi trans-sialidase, TS, catalytically active fragment TS 154.
ADC21529 standard; protein; 200 AA.
                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trypanosoma cruzi.
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                                                                                                                                    18-DEC-2003
                                                                    ADC21529;
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RESULT 7 ADC21529 26-SEP-2002.

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The invention relates to a T. cruzi trans-sialidase (TS) derived

CC neurotrophic peptide appearing as ADC21513 or ADC21511 called C44 and

CC (14, or its variant, and an interleukin-6 (IL-6) secretion inducing

CC oppride appearing as ADC21531 called TR-1 (terminal repeat 1). Also

CC comprising the peptides and a fusion partner, a composition comprising

CC comprising the peptides and a fusion partner, a composition comprising

CC defining therapeutically effective amount of T. cruzi trans-

CC daministering a therapeutically effective amount of T. cruzi trans-

CC an IL-6 inducing variant. The fusion partner comprising secretion of IL-6 (interleukin-6) in a mammal comprising administering TS

CC or an IL-6 inducing variant. The fusion partner comprises a mammalian

CC or an IL-6 inducing variant. The fusion partner comprises a mammalian

CC leukaemia inhibitory factor (LIF). The peptides are useful in providing

CC leukaemia thubitory factor (LIF). The peptides are useful in providing

CC condition selected from: amyotrophic lateral sclerosis, Alzheimer's

CC diesase, Parkinson's disease, Huntington's disease, Chagas 'disease,

CD eripheral neuropathy, palsies, multiple sclerosis, Alzheimer's

CD epripheral neuropathy, palsies, multiple sclerosis, Alzheimer's

CD epripheral neuropathy, palsies, multiple sclerosis, brain trauma,

CC catalytically active fragment TS 154.
                                                                                                                                                                                cruzi trans-sialidase derived neurotrophic and interleukin-6 secretion lucing peptides, useful in the treatment of neuronal degeneration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 KKKQVFSKIFYSEDEGKTWKFGEGRSDFGCSEPVALEWEGKLIINTRVDYRRLVYESSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 MGNSWVEAVGTLSRVWGPSPKSNQPGSQSSFTAVTIEGMRVMLFTHPLNFKGRWLRDRLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    catalytically inactive fragment TS H32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trans-sialidase; TS; neurotrophic peptide; interleukin-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.3%; Score 1067; DB 7;
100.0%; Pred. No. 2.7e-82;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                              Example 3; SEQ ID NO 30; 79pp; English.
                                                                                                                                                                                              inducing peptides, userus caused for example by Chagas' disease.
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                                                    99US-0172881P.
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                                                                                                                      Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.(
Matches 200, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                   Pereira
                                                                                                                                              WPI; 2003-786654/74.
                                                                                 (TUFT ) UNIV TUFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 200 AA;
                                               20-DEC-1999;
                                                                                                                   Chuenkova M,
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ADC21530
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181 KSVLQSWKNWDSHLSSICTP 200
                                                                                                                                                                                                                                                                                Trypanosoma cruzi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ29719
                                                                                                                                                                                                                                                                                                              W09960130-A1
                                                                                                                                                                                                                                                                                                                                                                               18-MAY-1999;
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                                                                                                                                               27-MAR-2000
                                                                                                                                                                                                                                                                                                                                               25-NOV-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Norris KA;
                                                                                                                 AAY44454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a 1. cruzi transferent case (12.) derived

neurotrophic peptide appearing as ADC21513 called (44 and
C14, or its variant, and an interleukin-6 (IL-6) secretion inducing
c14, or its variant, and an interleukin-6 (IL-6) secretion inducing
c15 peptide appearing as ADC21511 called TR-1 (terminal repeat 1). Also
c16 included are a composition comprising the peptides, fusion protein
c0 included are a composition comprising the fusion pratient, a composition comprising
c0 included are a partial a protein and comprising comprising the fusion protein and a physiological acceptable carrier, providing
c1 trophic support for neurons or glial calls in a mammal (comprising
c1 daministering a therapeutically effective amount of T. cruzi trans-
c2 sialidase (TS) or a neurotrophic variant) and stimulating (M3) the
secretion of IL-6 (interleukin-6) in a mammal comprising administering TS
c1 an IL-6 inducing variant. The fusion partner comprises a mammalian
c2 neurotrophic factor which is ciliary neurotrophic factor (CTF) or
leukaemia inhibitory factor (ILF). The peptides are useful in providing
c1 trophic support for neurons and glial calls in a mammal suffering a
condition selected from: amyotrophic lateral sclerosis, Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                              T. cruzi trans-sialidase derived neurotrophic and interleukin-6 secretion inducing peptides, useful in the treatment of neuronal degeneration caused for example by Chagas' disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease, Parkinson's disease, Huntington's disease, Chagas' disease, peripheral neuropathy, palsies, multiple sclerosis, stroke, brain trauma, spinal cord trauma and peripheral nerve trauma, and in stimulating the secretion of IL-6. The present sequence represents the trans-sialidase catalytically inactive fragment TS H32 (has 6 substitutions in the
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IL-6 secretion inducing peptide, neuron, glial cell; trophic support; cillary neurotrophic factor; CNTF; leukaemia inhibitory factor; LIF; amyotrophic lateral sclerosis; Albeimer, s disease; Parkinson's disease; Huntington's disease; Chagas' disease; peripheral neuropathy; palsy; multiple sclerosis; stroke; brain trauma; spinal cord trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KKKOVFSKIFYSEDDGKTWKFGEGRSAFGCSEAVALEWEGKLINTRVDYRRRLVYESSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1037; DB 7;
Pred. No. 9.6e-80;
4; Mismatches 2;
                                                                                  peripheral nerve trauma; mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; SEQ ID NO 31; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSVLQSWKNWDSHLSSICTP 418
                                                                                                                                                                                                                               20-DEC-2000; 2000US-00745008.
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Best Local Similarity 97.0%;
Matches 194; Conservative
                                                                                                                                                                                                                                                                                                                               Pereira MA;
                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-786654/74.
                                                                                                                                                                                                                                                                                               (TUFT ) UNIV TUFTS.
                                                                                                                                  Trypanosoma cruzi.
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                                                                                                                                                                                                                                                                                                                               Chuenkova M,
                                                                                                                                                                                                                                                               20-DEC-1999;
                                                                                                                                                                                                26-SEP-2002
                                                                                                                   Synthetic.
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53 SFRLPALVNVDGVMVAIADARYETSNDN-SLIDTVAKYSVDDGETWETQIAIKNSRAS-S 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 KVVŠLVILAKKTSYGWEFSNGTSDEGČIQPAVLEWKEKELIMMTSCDDGSRRVYRSSTWG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is Trypanosoma cruzi complement regulatory protein. This is encoded by a full length coding sequence from strain Y of T. cruzi. This sequence is used to construct a recombinant T. cruzi CRP enkaryotic expression cassette. Recombinant CRP produced from host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  can be used as a vaccine to prime the immune system of an animal. Hybridomas secreting monoclonal antibodies recognising CRP are produced. This is used to detect Chagas's disease-related proteins and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      new vector encoding Trypanosoma cruzi complement regulatory protein,
or treatment of Chaga's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVFSKIFYSEDEGKTWKFGEGRSDFGCSEPVALEW-EGKLIINTRVDYRRRLVYESSDMG
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                                                                                                                                                                                                                                                                                                                                             protein; CRP; vaccine;
                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma cruzi strain Y; Chagas' disease; recombinant CRP eukaryotic expression cassette.
                                                                                                                                                                                                                                                          cruzi complement regulating protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 21-25; 33pp; English.
AAY44454 standard; protein; 1003 AA.

    cruzi complement regulatory

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                                                                                                                                                                  (first entry)
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Matches 238; Conservative
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LLSSHS------ISHFYIGGDGKSSGNI-HVTVSNALLYNRLLQDDELNPLMKTKA 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T. cruzi complement regulatory protein; CRP; GPI anchor addition site;
mammalian decay accelerating factor gene; DAF; plasmid pBG12BI-CRP/DAF;
recombinant CRP eukaryotic expression cassette; Chagas' disease; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a modified Trypanosoma cruzi complement regulatory protein. The carboxy terminal end was modified to promote surface production in mammalian cells. The predicted GPI anchor addition site was removed and replaced with the C-terminal sequence of mammalian decay accelerating factor gene, which is recognised by mammalian cells. This was used in the construction of the plasmid pBC12BI-CRP/DAP for production of recombinant CRP in mammalian cells. Recombinant CRP
                                                            ---KDDKLYCLHEINSNE-VY
               VGFLSHSATKTEWEDAYRCVNAST-ANAERVPN-GLKFAGVGGGALWPVSQQGQNQRYHF
                                                                                                           ANHAFILVASVIIHEVPSVAS---PLLGASLDSSGGKKLLGLSYDEKHOWOPIY-GSTPV
                                                                                                                                                       --SGQTVVPDGRTPDISHFYVGGYGRSDMPTISHVTVNNVLLYNRQLNAEBIRTLFLSQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    new vector encoding Trypanosoma cruzi complement regulatory protein, or treatment of Chaga's disease.
                                                                                                                                                                                      TPTG----SWEMGKRYHVVLTMANKIG-SVYIDG------EPLEG
                                             SLVFARLVGELRIIKSVLOSWKNWDSHLSSICTPADPAASSSER----
                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified T. cruzi CRP with C-terminal mammalian DAF,
WLTDNORIYNVGQVSIGDENSAYSSVLY-
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                                                                                                                                                                                                                                                                                    LIGTEAHMGSSSGSSERSTPG
                                                                                                                                                                                                                                                                                                   100 VAASEAEVSAPEGAPQNSHLG
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produced from host cells can be used as a vaccine to prime the immune system of an animal. Hybridomas secreting monoclonal antibodies recognising CRP are produced. This is used to detect Chagas's diseaserelated proteins and for treatment of the disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGFLSHSATKTEWEDAYRCVNAST-ANAERVPN-GLKFAGVGGGALWPVSQQGQNQRYHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                470 VGLLSNKSTKNTWSDEYLCVNATVHGEVESAPDGGLTFKGPGAGAKWPVGDMGQTVPYHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANHAFTLVASVTIHEVPSVAS---PLLGASLDSSGGKKLLGLSYDEKHQWQPIY-GSTPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LISSHS-----ISHFYIGGDGKSSSGNI-HVTVSNALLYNRLQDDELNPLMKTKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SGQTVVPDGRTPDISHFYVGGYGRSDMPTISHVTVNNVLLYNRQLNAEBIRTLFLSQD
                                                                                                                                                                                                                                                  85;
                                                                                                                                                                                   25.7%; Score 903; DB 3; Length 1006; 34.9%; Pred. No. 3e-67; 1ve 88; Mismatches 270; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trypanosome; trans-sialidase; neuramidase; sleeping sickness;
Chagas' Disease; parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      554 TPTG----SWEMGKRYHVVLIMANKIG-SVYIDG------EPLEG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trans-sialidase/neuramidase encoded by clone 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIGTEAHMGSSSGSSERSTPG 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : : | | : | : | | | VAASEAEVSAPEGAPQNSHLG 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
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                                                                                                                                                                                                                                          Conservative
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(first entry)
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238; Conserv
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                                                                                                                                Sequence 1006 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
26-APR-1994
                                                                                                                                                                           Query Match
Best Local S
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ID AAR4
XX AC AAR4
XX DT 25-h
DT 26-j
XX XX Tryj
XX Tryj
XW Tryj
KW Chae
  8X8888
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RVDYRRRLVYESSDMGNSWVBAVGTLSRVWGPSPKSNQPGSQSSFTAVTIEGMRVMLFTH 120
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                                                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid sequence of the portion of trans-sialidase which imparts trans-sialidase and/or neuramidase activity. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 ASNGNLVYPVQVTNKKKQVFSKIFYSEDEGKTWKFGEGRSDFGCSEPVALEWEGKLIINT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ASNGNLVYPVQVTNKKKQVFSKIFYSEDEGKTWKFGEGRSDFGCSEPVALEWEGKLINT
                                                                                                                                                                                                                                                                                                      New trans-sialidase polypeptide(s) isolated from Trypanosoma - used for transferring sialic acid or for treating or preventing trypomastigote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      some; trans-sialidase; neuramidase; sleeping sickness;
Disease; parasite.
                                                                                                                                                                                                                    Vandekerckhove F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.1%; Score 884; DB 2; Length 166; 100.0%; Pred. No. 7.6e-67; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLNFKGRWLRDRLNLWLTDNQRIYNVGQVSIGDENSAYSSVLYKDD 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trans-sialidase/neuramidase encoded by clone 121/151.
/note= "corresponds to CTA codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "corresponds to CTA codon"
                                                                                                                                                                                                                      Nussenzweig V, Schenkman S, Eichinger D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR42015 standard; protein; 166 AA
                                                                                                                                                                                                                                                                                                                                                                           Claim 15, Fig 18; 130pp; English.
                                                                                                 93WO-US002869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93WO-US002869
                                                                                                                                   92US-00857519
92US-00973851
                                                                                                                                                                                   (UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                      WPI; 1993-320452/40.
N-PSDB; AAQ49594.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                   25-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-1993;
                                 WO9318787-A1
                                                                                                                                   25-MAR-1992;
10-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9318787-A1
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                                                                   30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chagas,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVDYRRRLVYESSDMGNSWVEAVGTLSRVWGPSPKSNQPGSQSSFTAVTIEGMRVMLFTH 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVDYRRRLVYESSDMGNSWVEAVGTLSRVWGPSPKSNQPGSQSSFTAVTIEGMRVMLFTH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clones 121 and 151, isolated from T.cruzi DNA library by homology to known neuramidase sequences, were found to have identical sequences in the region of the trans-sialidase gene necessary for enzymatic activity. The 121/151-encoded amino acid sequence (AAR42015) is similar to the known TCNA sequence (AAR42016) but distinct from the sequence encoded by clone 154 (AAR42017). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ASNGNLVYPVQVTNKKKQVFSKIFYSEDEGKTWKFGEGRSDFGCSEPVALEWEGKLINT
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Chagas' Disease; parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135.1%; Score 884; DB 2; Length 166; ilarity 100.0%; Pred. No. 7.6e-67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLNFKGRWLRDRLNLWLTDNQRIYNVGQVSIGDENSAYSSVLYKDD 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vandekerckhove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein with trans-sialidase and/or neuramidase activity.
                                                                                 /note= "corresponds to CTA codon"
                                                                                                                                                                                                                                                                                                          Eichinger D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key Location/Qualifiers
Misc-difference 149
                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 23; 130pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR42014 standard; protein; 166 AA
                                                                                                                                                                                                                      92US-00857519.
92US-00973851.
                                                                                                                                                                                                                                                                                                        Nussenzweig V, Schenkman S,
                                                                                                                                                                                      93WO-US002869
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                                                                                                                                                                                                                                                                                                                                             WPI; 1993-320452/40.
                                                                     Misc-difference 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Тгураповоща сгиzi.
                   Trypanosoma cruzi
                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ49597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 166 AA;
                                                                                                                                                                                      25-MAR-1993;
                                                                                                                                                                                                                        25-MAR-1992;
10-NOV-1992;
                                                                                                                     WO9318787-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR42014;
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Clones 121 and 151, isolated from T.cruzi DNA library by homology to thown neuramidase sequences, were found to have identical sequences in the region of the trans-stalidase gene necessary for enzymatic activity. The 121/151-encoded amino acid sequence (AAR42015) is similar to the known TCNA sequence (AAR42016) but distinct from the sequence encoded by clone 154 (AAR42017). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                           New trans-sialidase polypeptide(s) isolated from Trypanosoma - used for transferring sialic acid or for treating or preventing trypomastigote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing Trypanosoma cruzi infection by detecting antibodies to novel antigens - which are useful in vaccines to provide protective immunity against Chagas' disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 ASNGNLVYPVQVTNKKKQVFSKIPYSEDEGKTWKFGEGRSDFGCSBPVALEWEGKLIINT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 RVDYRRRLVYESSDMGNSWVEAVGTLSRVWGPSPKSNQPGSQSSFTAVTIEGMRVMLPTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epitope; vaccine; protective immunity; Chagas disease;
                       Vandekerckhove F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLNFKGRWLRDRLNLWLTDNQRIYNVGQVSIGDENSAXSSVLYKDD 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 825; DB 2;
Pred. No. 8e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lodes MJ, Houghton RL;
                     Eichinger D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 88-91; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma cruzi; Tulahean strain C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; protein; 618 AA.
                                                                                                                                                                                                                      Claim 22; Fig 23; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; therapy; immunoassay
                   Schenkman S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.5%;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky YAW,
                                                             1993-320452/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-289413/26.
N-PSDB; AAT69167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP
                                                                                N-PSDB; AAQ49596
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 166 AA;
                   Nussenzweig V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-NOV-1996;
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12-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen;
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                셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVDYRRRLVYESSDMGNSWVEAVGTLSRVWGPSPKSNQPGSQSSFTAVTIEGMRVMLFTH 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                           Clones 121 and 151, isolated from T.cruzi DNA library by homology to known neuramidase sequences, were found to have identical sequences in the region of the trans-sialidase gene necessary for enzymatic activity. The 121/151-encoded amino acid sequence (AAR42015) is similar to the known TCNA sequence (AAR42016) but distinct from the sequence encoded by clone 154 (AAR42017). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                          New trans-sialidase polypeptide(s) isolated from Trypanosoma - used for transferring sialic acid or for treating or preventing trypomastigote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ASNGNLVYPVQVTNKKKQVFSKIFYSEDDGKTWKFGEGRSAFGCSEAVALEWEGKLIINT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 24.3%; Score 854; DB 2; Length 166; Best Local Similarity 96.4%; Pred. No. 2.7e-64; Matches 160; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLNFKGRWLRDRLNLWLTDNQRIYNVGQVSIGDENSAYSSVLYKDD 370
                                                                                                                    Vandekerckhove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "corresponds to CTA codon"
                                                                                                                    Eichinger D,
                                                                                                                                                                                                                                                                                                                     Disclosure, Fig 23; 130pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCNA Trans-sialidase/neuramidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR42016 standard; protein; 166
                                                                                                                  Schenkman S,
    92US-00857519
92US-00973851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosome; trans-sialidase;
                                                                (UYNY ) UNIV NEW YORK STATE
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92US-00973851
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chagas' Disease; parasite
                                                                                                                                                          WPI; 1993-320452/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trypanosoma cruzi.
                                                                                                                                                                                    N-PSDB; AAQ49595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 166 AA;
                                                                                                               Nussenzweig V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Misc-difference
25-MAR-1992;
10-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9318787-A1
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10-NOV-1992;
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26-APR-1994
                                                                                                                                                                                                                                                                            infection.
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264

9

This polypeptide sequence comprises a full-length antigen of Trypanosoma cruzi, identified by sequencing a DNA clone (see AAT65167) obtained by screening a Trypanosoma cruzi genomic expression library with pools of sera from infected individuals. T. cruzi antigens (see AAW25530-41), or AAW26542-44) of native antigens, can be used in a variety of immunoassays for detecting T. cruzi infection in a blood, serum, plasma, saliva, cerebrospinal fluid or urine sample. The polypetides are also useful in vaccines and pharmaceutical compositions for inducing protective immunity against Chagas disease. They can be produced by expression in transformed or transfected host cells. (Updated on 17-OCT-2003 to standardise OS field) X88888888888888888888888

Sequence 618 AA;

47 TERVVHSFRLPALVNVDGVMVAIADARYETSNDNSLIDTVAKYSVDDGETWETQIAIKNS 106 GVFLVELVDAASGTIRTREKMQPTTIVSGDTIYMALGDYEKK----TSGGRAADADGWRL 137 184 262 185 TKNGYLVLPMQAVEKDGRSVVLSMRFNMRIE--ACELSSGTTGSNCKEPSIANLEGNLIL 242 322 243 ITSCAAGYYEVFRSLDSGISWEMSGRPISRVWGNSYGQKGYGVRCGLITVTIEGREVLLV 302 381 303 TIPVYLEEKNGRGRLHLMVTDGARVHDAGPISDAADDAAASSLLYSSGGNLISLYENKSE 362 438 418 497 478 553 909 -----RASSVSRV---VDPTVIVKGNKLYVLVGSYNSSRSYWTSHG---DARDWDI 151 LLAVGEVTKSTAGGKITASIKWGS-----PVSLKEFFPAEMEGMHTNQFLGGAGVAIV 204 81 SEAAAGSLCVPSLAEVAGGVFAVAEAQRSERDEACGHAAIATTHIETGGGGSKAISAMDA 205 ASNGNLVYPVQVTNK--KKQVFSKIFYSEDEGKTWKFGEGRSDFGCSEPVALEWEGKLII NTRVDYRRRLVYESSDMGNSWVEAVGTLSRVWGPSPKSNQPGSQSSFTAVTIEGMRVMLF THPLNFKGRWLRDRLNLWLTDNQRIYNVGQVSIGDENSAYSSVLYKD-DKLYCLHEINSN 363 GSYGLVAVHVTTQLERIKTVLKRWQELDEALRTCRSTATIDPV----RRGMCIRPILLTDG 498 ANHAPTLVASVTIHEVPSVAS--PLLGASLDSSGGKKLLGLSYDEKHQWQPIY--GSTPV 554 TPTGSWEMGKRYHVVLTMANKIGSVYIDGE----PLEG--SGQTVVPDGRTPDISHFYV 382 EVYSLVFARLVGELRIIKSVLQSWKNWDSHLSSICTPA--DPAASSSERG-CGPAVTTVG LVGFLSHSATKTEWEDAYRCVNASTANAER-VPNGLKFAGVGGGLWPVSQQGQNQRYHP 71; Gaps Length 618; 84; Mismatches 268; Indels / Match 18.0%; Score 631.5; DB 2; Local Similarity 31.0%; Pred. No. 1.8e-44; nes 190; Conservative 84; Mismatches 268; GGYGRSDMPTISH 619 107 82 152 263 323 607 Query Match Best Loca Matches 셤 g g g g g 엄 ద g ઠે δ ઠે ઠ ઠ 8 ઠ ð g ò

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Enkaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Enkaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.

1 (bases 1 to 629)
Munden, H., Nelsan, S., Pazelinia, G., Mack, J., Marty, A.,
Munden, H., Nelsan, S., Pentony, M., Rinta, J., Robertson, L.,
Seyler, A., Sisk, B., Stuart, K., Vogt, C., Worthey, E., El-Sayed, N.M.,
Ghedin, E. and Andersson, B.
Trypanosoma cruzi CL-Brener TC3 BAC-end sequencing
Unpublished (2001)
Other GSSs: TC3-53G11.TV
Contex: Peter Wyler
Seattle Blomedical Research Institute
4 Nickerson Street, Seattle, WA 98109, USA
Tel: 206 284 8846
Fax: 206 284 0313
Email: mylerpj@sbri.org
Clones are derived from the Trypanosoma cruzi CL-Brener BAC library
BH844084 TC3-53M19
BH8442621 TC3-53123
BH197094 TC3-73F9.
BH8444627 TC3-50N19
BH8444823 TC3-50N13
BH844385 TC3-51M23
AQ91119146 TC3-51M23
AQ91119146 TC3-51M23
AQ91119146 TC3-51M23
AQ910653 GSSTC0128
AQ907246 GSSTC0128
AQ907246 GSSTC0128
AQ907246 GSSTC0128
AQ907246 GSSTC0128
BH844302 TC3-52A3.
BH843018 TC3-52A3.
BH19504 TC3-74H19
BH19502 TC3-74H19
BH19502 TC3-77F7.
BH19504 TC3-76H13
BH19524 TC3-76H19
BH19525 TC3-11E11
AQ953466 Sheared D
BH19495 TC3-10C3.
BH194731 TC3-50K13
BH194744 TC3-50K13
BH19474 TC3-50K13
BH19477 TC3-50K13
BH1941354 TC3-50K13
AQ953610 Sheared D
BH191354 TC3-50K13
AQ951915 Sheared D
AL472697 TC3-50K13
AQ951915 Sheared D
AL472697 TC3-50K13
BH844180 TC3-50G15
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                                                                                                                                                                                                                                                           AQ953610
TA155F11Q
AQ940568
BH191354
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BH844385
BH844385
AQ91046
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AZ302499
AA556106
BH84222
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AQ953264
BH193191
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AQ951915
TA19G08P
AQ946989
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BH844627
BH843788
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BH846083
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BH844958 TC3-53G7.
BH844398 TC3-56J15
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553.4
551.2
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                                                                                                               Sequence:
                                                                                                                                                         Searched:
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                                                             Run on:
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No.
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/db_xxef="toxon:569a"
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/clone="Tc2-568e"
/clone="Tc2-68e"
/clone="Tc
                                                                 672 bp DNA linear GSS 13-JUN-2002 TC3 Trypanosoma cruzi genomic clone TC3-56E8, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mylerpjøsbri.org
Clones are derived from the Trypanosoma cruzi CL-Brener BAC library
TC3. For clone availability, please contact Dr. Bjorn Andersson at
Uppsala University (bjorn.andersson@genpat.uu.se).
Seg primer: T7
                                                                                                                                                                                                                                                                                                              L UdaBes I to b/2/
Myler, D.'. Aggarwal, G., Fazelinia, G., Mack, J., Marty, A.,
Munden, H., Nelson, S., Pentony, M., Rinta, J., Robertson, L.,
Seyler, A., Sisk, B., Stuart, K., Vogt, C., Worthey, E., El-Sayed, N.M.,
Ghedin, E. and Andersson, B.
Trypanosoma cruzi CL-Brener TC3. BAC-end sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAATACAACTGTGAGTATCAAATGGGGGGGCCCCGTCCCAGTGAAGGAATTTTTCCCTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 AIGCGAGAGACTGGGGATATTCTGCTTGCGGTGGGGGTCACGAAGTCCACTGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ArdccaAcraGaArrarrcracrraccarracraArarcacaAgracacacara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 AGCTTTACGTCCTGGTTGGAAGCTACAACAGTTCGAGGAGGTACTGGACGTCGCATGGTG
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                                                                                                                                                                                                                              Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 672)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Other GSSs: TC3-568.TP
Other GSSs: TC3-568.TP
Contact: Peter Myler
Seattle Biomedical Research Institute
A Nickerson Street, Seattle, WA 98109,
Tel: 206 284 8846
Fax: 206 284 0313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cruzi"
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/organism="Trypanosoma c
/mol_type="genomic DNA"
/strain="CL Brener"
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                                                                                                                                                           BH841269.1 GI:21408484
                                                                                                                                                                                                          Trypanosoma cruzi
                                                                                                              survey sequence.
BH841269
                                                            BH841269
TC3-56E8.TV
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Best Local Similarity
Matches 617; Conserv
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AUTHORS
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JOURNAL
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                                                                                                                                  TC3. For clone availability, please contact Dr. Bjorn Andersson at Uppsala University (bjorn.andersson@genpat.uu.se).
Seq primer: SP6
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTGTGTACCCTGTGCAGGTTACGAACAAAAGAAGCAAGTTTTTTCCAAGATCTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTGTGTACCCTGTGCAGGTTACGAACAAAGGAAGCAAGTTTTTTCCAAGATCTTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       688 TCGGAAGACGAGGCAAGACGTGGAAGTTTGGGGAGGGTAGGAGTGATTTTGGCTGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAACCTGTGGCCCTTGAGTGGGAGGGGGAAGCTCATAAACACTCGAGTTGACTATCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCTCACGTGTGTGGGGCCCCTCACCAAAATCGAACCAGCCGGGCAGTCAGAGCAGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 29.4%; Score 590.6; DB 28; Length 629; Best Local Similarity 98.3%; Pred. No. 3.1e-149; Matches 618; Conservative 0; Mismatches 9; Indels 2;
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du Polymorphisme Humain (CEPH), Paris, France. Briefly, Trypanosoma cruzi (C.Brener agarose embedded DNA (bhtained from Dr. Franco da Silveira) was partially digested with Hin dIII. High molecular weight fragments were ligated in BabeloBACII digested with Hin dIII. The average insert size is 1100 kb. Total clone coverage: approx. 33 X the haploid genome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                652 bp DNA linear GSS 13-JUN-2002
TC3-56115.TV TC3 Trypanosoma cruzi genomic clone TC3-56115, genomic
BH844398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      958 ATGCTCTTCACACACCCGCTGAATTTTAAGGGAAGGTGGCTGCGCGACTGAACCTC 1017
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                                                                                                                                                                                                                                                                                                                                AAGGAATTTTTCCCGGCGGAAATGGAAGGAATGCACACAAATCAATTTCTTGGCGGTGCA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCATCATAAACACTCCGAGTTGACTATCGCCGCCGTCTGGTGTACGAGTCCAGTGACATG 418
                                                                                                                                                                                                                                                                                                         478 AAGTCCACTGCGGGCGAGGTAACTGCGAGTATCAAATGGGGGAGCCCCGTGTCACTG 537
                                                                                                                                                                                                                                                                                                                                                                              AAGGAATITITICCCGGCGGAAATGGAAGGAATGCACACAAATCAATITICTIGGCGGTGCA 597
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                                                                                                                                                                                                                                                         CTCATCATAAACACTCGAGTTGACTATCGCCGCCGTCTGGTGTACGAGTCCAGTGACATG
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 652)
Myler, P.J., Aggarwal, G., Fazelinia, G., Mack, J., Marty, A., Munden, H., Nelson, S., Pentony, M., Rinta, J., Robertson, L.,
                                                                                                                                                                Length 599;
                                                                                                                                                                                                 21; Indels
                                                                                                                                                                DB 28;
                                                                                                                                                            Score 553.4; DB 28
Pred. No. 4.1e-139;
0; Mismatches 21;
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                                                                                                                                                                27.5%;
                                                                                                                                                                                  Best Local Similarity 96.2
Matches 578; Conservative
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genomic clone TC3-53G7, genomic
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Trypanosoma cruzi

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma; Schizotrypanum.

I (bases 1 to 599)

Myler, P.J., Aggarwal, G., Fazelinia, G., Mack, J., Marty, A.,

Munden, H., Nelson, S., Pentony, M., Rinta, J., Robertson, L.,

Ghedin, E. and Andersson, B.,

Trypanosoma cruzi CL-Brener TC3 BAC-end sequencing

Unpublished (2001)

Other GSSS: TC3-53G'.TP
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   CGTCCAACGGGAATCTTGTGTACCCTGTGCAGGTTACGAACGTGAAGGGACAAATTTTCT 300
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/clone lib="TC3"
/note="Wector: pBelOBAC11; Site_1: Hin dIII; Constructed for Uppsala University by Marie-Christine Le Paslier in the laboratory of Denis Le Paslier at the Centre d'Etude
                                                         CCAAGATCTTCTACTCGGAAGATGATGGCAAGACGTGGAAGTTTGGGAAGGTAAGGAGCG
                                                                                                                                CTTTTGGCTGCTGTGAACCTGTGGGCCCTTGAGGGGAAGGCTCATCATAAACACTC
                                                                                                                                                                                  AGGCTGTCGGCACGCTCTCACGTGTGTGGGGCCCCTCACCAAAATCGAACCAGCCCGGCA
                                                                                                                                                                                                                                                                                         AGGCTGTCGGCACGCTCTCACGTGTGTGGGGCCCCTCACCAAAATCGGACCAGCCCGGCA
                                                                                                                                                                                                                                                                                                                          GTCAGAGCAGCTTCACTGCCGTGACCATCGAGGAATGCGTGTTATGCTCTTCACACACC
                                                                                                                                                                                                                                                                                                                                               GTCAGAGCAGCTTCACTGCCGTGACCATCGAAGGAATGCGTGTGAATGCTCTTCACACACC
                                     CCAAGATCTTCTACTCGGAAGACGAGGGCAAGACGTGGAAGTTTGGGGAGGGTAGGAGTG
                                                                                                             734 ATTTTGGCTGCTCTGAACCTGTGGCCCTTGAGTGGGAGGGGAAGGTCATCATAAACACTC
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4 Nickerson Street, Seattle, WA 98109,
Tel: 206 284 8846
Fax: 206 284 0113
Email: mylerpj@sbri.org
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TC3-53G7.TV TC3 Trypanosoma cruzi
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/mol_type="genomic DNA"
/strain="CL Brener"
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1. .599
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/db_xref="taxon:5693"
/clone="Tc3-53M19"
/clone="Tc3-53M19"
/clone="Tc3-53M19"
/clone="Tc3-53M19"
/clone="Tc3-53M19"
/clone=Lib="Tc3-53M19"
/note="Vector: pBeloBAC11; Site 1: Hin dIII; Constructed for Uppsala University by Marie-Christine Le Paslier in the laboratory of Denis Le Paslier at the Centre d' Etude du Polymorphisme Humain (CEPH), Paris, France. Briefly, Trypanosoma cruzi (CI-Brener agarose embedded DNA (obtained from Dr. Franco da Silveira) was partially digested with Hin dIII. High molecular weight fragments were ligated in pBeloBAC11 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 33 X the haploid genome."
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Eukaryota; Englencoza; Kinetoplastida; Trypanosomatidae;

Enkaryota; Englencoza; Kinetoplastida; Trypanosomatidae;

Trypanosoma; Schizotrypanum.

E 1 (bases 1 to 675)

S Myler, P. J. Aggarwal, G., Fazelinia, G., Mack, J., Marty, A., Muden, H., Nelson, S., Pentony, M., Rinta, J., Robertson, L., Seyler, A., Sisk, E., Stuark, K., Vogt, C., Worthey, E., El-Sayed, N.M., Sayler, M., Sisk, E., Stuark, K., Vogt, C., Worthey, E., El-Sayed, N.M., Trypanosoma cruzi CL-Brener TC3 BAC-end sequencing

Unpublished (2001)

Unpublished (2001)

Cothac GSSs: TC3-S3M19.TP

Contact: Peter Myler

Seattle Biomedical Research Institute

4 Nickerson Street, Seattle, WA 98109, USA

Tel: 206 284 8846
                                                                                                                                                                                                                                                                                                                                                       DNA linear GSS 13-JUN-2002
genomic clone TC3-53M19, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mylerpjøsbri.org
Clones are derived from the Trypanosoma cruzi CL-Brener BAC library
TC3: For clone availability, please contact Dr. Bjorn Andersson at
Uppsala University (bjorn.andersson@genpat.uu.se).
Seq primer: T7
Class: BAC ends.
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     Gapa
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/organism="Trypanosoma (
/mol_type="genomic DNA"
/strain="CL Brener"
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                                                                                                                                                                                                                                      Email: mylerpj@sbri.org
Clones are derived from the Trypanosoma cruzi CL-Brener BAC library
TC3. For clone availability, please contact Dr. Bjorn Andersson at
Uppsala University (bjorn.andersson@genpat.uu.se).
Class: BAC ends.
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Seyler, A., Sisk, E., Stuart, K., Vogt, C., Worthey, E., El-Sayed, N.M.,
Ghedin, E. and Andersson, B.
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Pred. No. 1.7e-138;
0; Mismatches 63; Indels 0;
                                           Trypanosoma cruzi CL-Brener TC3 BAC-end sequencing Unpublished (2001)
Unpublished (2001)
Cohter_GSSs: TC3-SGJ15.TP
Cohtact: Peter Myler
Seattle Blomedical Research Institute
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .652
/organism="Trypanosoma cruzi"
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/strain="CL Brener"
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/clone_lib="TC3"
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                                                                                                                                                                                             Tel: 206 284 8846
Fax: 206 284 0313
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Matches 589; Conservative
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8 셤 ò 셤 δ 셤 à 셤 ò g ð 쉽 à ద ò 셤

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BH197094 495 bp DNA linear GSS 24-OCT-2001 TC3-73F9, TV TC3 Trypanosoma cruzi genomic clone TC3-73F9, genomic survey sequence.
BH197094.1 GI:16365250
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               Location/Qualifiers
1. .532
/organism="Trypanosoma
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Clones are derived from the Trypanosoma cruzi CL-Brener BAC library
TC3: For clone availability, please contact Dr. Bjorn Andersson at
Uppsala University (bjorn.andersson@genpat.uu.se).
Seq primer: SP6
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                                             GCAAGATAACTGCGAGTATCAAATGGGGGAGCCCCGTGTCACTGAAGGAATTTTTCCCGG
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TC3-53123.TP TC3 Trypanosoma cruzi
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/db_xrefe="rc3" should be been as a part of the ball o
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TC3-50N19.TV TC3 Trypanosoma cruzi genomic clone TC3-50N19, genomic
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Trypanosoma cruzi
Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizctrypanum.

1 (bases 1 to 526)
Myler, P. J., Aggarwal, G., Fazelinia, G., Mack, J., Marty, A., Sayler, P., Seyler, A., Sisk, E., Stuart, K., Vogt, C., Worthey, E., El-Sayed, N.M., Trypanosoma cruzi CL-Brener TC3 BAC-end sequencing
Unpublished (2001)
Other GSSS: TC3-50N19.TP TC3-50N19.TP.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: myletpj@sbri.org
Clones are derived from the Trypanosoma cruzi CL-Brener BAC library
TC3. For clone availability, please contact Dr. Bjorn Andersson at
Uppsala University (bjorn.andersson@genpat.uu.se).
Seg primer: T7
Class: BAC ends.
                  493
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Pred. No. 1e-113;
0; Mismatches 40; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Peter Myler
Scattle Biomedical Research Institute
4 Nickerson Street, Seattle, WA 98109, USA
Tel: 206 284 8846
Fax: 206 284 0313
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22.9%;
Best Local Similarity 92.4%;
Matches 484; Conservative
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                                                                                                                                                                                              Other GSSs: TC3-73F9.TP
Contact: Bjorn Andersson
Department of Genetics and Pathology
Uppsala University,
Rudbeck Laboratory, SE-751 85, Uppsala, Sweden
Tel: 46 18 471 4807
Fax: Accordance are derived from the Trypanosoma cruzi CL-Brener BAC library
TC3. For clone availability, please contact Dr. Bjorn Andersson at
Uppsala University (bjorn.andersson@genpat.uu.se).
Seq primer: T7
Class: BAC ends.
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/clone="TC3-73F9"
/clone="TC3-73F9"
/clone="TC3-73F9"
/clone="TC3-73F9"
/note="Vector: pBeloBAC11; Site_1: Hin dIII; Constructed for Uppsala University by Marie-Christine Le Paslier in the laboratory of Denis Le Paslier at the Centre d'Etude du Polymorphisme Humain (CEPH), Paris, France. Briefly, Trypanosoma cruzi CL-Brener agarose embedded DNA (obtained from Dr. Franco da Silveira) was partially digested with Hin dIII. High molecular weight fragments were ligated in pBeloBAC11 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 33 X the haploid genome."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GGCAAGATAACTGCGAGTATCAAATGGGGAGCCCCGTGTCACTGAAGAATTTTTCCCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               612
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                           1 (bases 1 to 495)
Kluge, S., Edwards, K.E., Nilsson, D., Bontempi, E.J., Myler, P., Stuart, K., Ghedin, E., El-Sayed, N.M. and Andersson, B.
Clustering and analysis of BAC-end and GSS sequences from Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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Pred. No. 1.2e-120;
0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cruzi"
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/organism="Trypanosoma «
/mol_type="genomic DNA"
/strain="CL Brener"
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Trypanosoma; Schizotrypanum
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llarity 98.8%;
Conservative 0
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Clones are derived from the Trypanosoma cruzi CL-Brener BAC library
TC3. For clone availability, please contact Dr. Bjorn Andersson at
Uppsala University (bjorn.andersson@genpat.uu.se).
Seg primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                             CCAACGGGAATCTTGTGTACCCTGTGCAGGTTACGAACATGAAAAAGAGCTTTTCTCCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGTCGGCACGCTCTCGCGTGTGTGGGGCCCCTCACCAAAATCGGACCAGCCCGGCAGTC 360
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Bukaryotsa, Euglenozoa, Kinetoplastida, Trypanosomatidae;
Trypanosoma, Schizotrypanum.
1 (bases i to 467).
Wyler, P.J., Aggarwal, G., Fazelinia, G., Mack, J., Marty, A.,
Munden, H., Nelson, S., Pentony, M., Rinta, J., Robertson, L.,
Seyler, A., Sisk, E., Stuart, K., Vogt, C., Worthey, E., El-Sayed, N.M.,
Ghedin, E. and Andersson, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGGCIGCICIGAACCIGIGGCCCITGAGIGGGAGGGGAAGCICAICAIAAACACICGAG 796
pBeloBAC11 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 33 X the haploid genome."
                                                                                                                                                                                                                                                                                                                                                       CTGTCGGCACGCTCTCACGTGTGTGGGGCCCCTCACCAAATTCGAACCAGCCCGGCAGTC
                                                                                                                                                                                                     ACATGGAAGGAATACCCACAAAAGCAATTTCTT-TTTTTTCAGGTGTTGCCACTGTGGCGGT
                                                                                                                                                                                                                                                         CCAACGGGAATCTTGTGTACCCTGTGCAGGTTACGAACAAAAAGAAGCAAGTTTTTTCCA
                                                                                                                                                                                                                                                                                                                                 AGATCTTCTACTCGGAAGACGAGGCAAGACGTGGAAGTTTGGGGGAGGTAGGAGTTGATT
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                                                                                                   Length
                                                                                                 Score 378.2; DB 28; Length
Pred. No. 1.8e-91;
0; Mismatches 48; Indels
                                                                                               DB 28;
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Tel: 206 284 8846
Fax: 206 284 0313
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Other GSSs: TC3-51M23.TV
Cottact: Peter Myler
Seattle Biomedical Research Institute
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BH843853
BH843853.1 GI:21412781
                                                                                                 Query Match
Best Local Similarity 89.5%;
Matches 418; Conservative
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Trypanosoma; Schizotrypanum.

Trypanosoma; Schizotrypanum.

Trypanosoma; Schizotrypanum.

Sa (barana) (Schizotrypanum.

Sa (barana) (Schizotrypanum.

Mundan, H., Nelson, S., Pentony, M., Rinta, J., Robertson, L., Sayler, A., Sisk, E., Stuart, K., Vogt, C., Worthey, E., El-Sayed, N.M., Ghedin, E. and Andersson, B.

Trypanosoma cruzi (L.-Brener TC3 BAC-end sequencing

Trypanosoma cruzi (L.-Brener TC3 BAC-end sequencing

Umpublished (2001)

Other_GSSs: TC3-51MC3.TV.1

Contact: Peter Mylez

Seattle Biomedical Research Institute

4 Nickerson Street, Seattle, WA 98109, USA

Tel: 206 284 8846

Fax: 206 284 8846

Fax: 206 284 8846

Trypanosoma cruzi (L.-Brener BAC library)

TC3. For clone are derived from the Trypanosoma cruzi (L.-Brener BAC library)

TC3. For clone availability, please contact Dr. Bjorn Andersson at Uppsala university (bjorn.andersson@genpat.uu.se).

Seq primer: T7

Class: BAC ends.
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/clone="TC3-51M23"
/clone="TC3-51M23"
/clone="Voctor: pBeloBAC11; Site 1: Hin dIII; Constructed for Uppsala University by Marie-Christine Le Paslier in the laboratory of Denis Le Paslier at the Centre d'Etude du Polymorphisme Humain (CBPH), Paris, France. Briefly, Trypanosoma cruzi Cl-Brener agarose embedded DNA (obtained from Dr. Franco da Silveira) was partially digested with Hin dIII. High molecular weight fragments were ligated in
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TC3-51M23.TV TC3 Trypanosoma cruzi genomic clone TC3-51M23, genomic
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       GCAAGACAACTGCGAGCATCAAATGGGGGAGCCCCGTGTCACTGAAGAAGTTTTTTCCGG 180
                                                             181 CAGAAATGGAAGGAATGCACACAAATCAATTTCTTGGGGGTGTGGGGGTGTTGCCATTGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="CL Brener"
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/organism="Trypanosoma
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On Sep 14, 2000 this sequence version replaced gi:9370791.
Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
AN. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos
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TC3-40G16.TF TC3 Trypanosoma cruzi genomic clone TC3-40G16, genomic BH191346
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Tel: (54-11) 4580/7255/7
Fax: (54-11) 4725-9639
Email: dsanchez@ilb.unsam.edu.ar
Sequences ware basecalled with phred and vector was masked with crossmatch (see http://genome.washington.edu). Sequences were thtrimmed from both ends to remove low quality bases and masked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AACCTGTGGCCCTTGAGTGGGAGGGGAAGCTCATCATAAACACTCGAGTTGACTGGACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="epimastigote"
/clone_lib="Trypanosoma cruzi random genomic library"
/note="Vector: pBS(-) (Stratagene); T. cruzi DNA was mandomly sheared using a nebulizer and the 1 to 2 KD was gel purified and cloned into the dephosphoryated Hincil site of the vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           869 TCTCACGTGTGGGGCCCCTCACCAAAATCGAACCAGCCCGGGAGTCAGAGCAGCTTCA
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18.5%; Score 372; DB 28;
Best Local Similarity 93.9%; Pred. No. 8.2e-90;
Matches 387; Conservative 0; Mismatches 25;
               gene discovery
) (12), 1996-2005 (2000)
                                                                                                                                                                                                                                                                                                                                                                         1. .412
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/strain="CL-Brener"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:5693"
/clone="G40M7"
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           families, and ge
Genome Res. 10 (
20568489
11116094
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                                                                                                   /clone="TC3-51M3"."
/clone="TC3-51M3"."
/clone lib="TC3"
/clone lib="TC3"
/clone lib="TC3"
/note="Vector: pBeloBAC11; Site 1: Hin dIII; Constructed for Uppsala University by Marie-Christine Ie Paslier in the laboratory of Denis Le Paslier at the Centre d'Etude du Polymorphisme Aumain (CEPH), Paris, France. Briefly, Trypanosoma cruzi (L-Brener agarose embedded DNA (obtained from Dr. Franco da Silveira) was partially digested with Hin dIII. High molecular weight fragments were ligated in pBeloBAC11 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 33 X the haploid genome."
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 412)
Aguero,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.
A random sequencing approach for the analysis of the trypanosoma cruzi genome: general structure, large gene and repetitive DNA
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GSSTG03225 Trypanosoma cruzi random genomic library Trypanosoma
cruzi genomic clone G40M7, genomic survey sequence.
AQ911191
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                                                                                                                                                                                                                                                                                                                                                          cch 18.8%; Score 378.2; DB 28; Length 467; al Similarity 89.5%; Pred. No. 1.8e-91; 418; Conservative 0; Mismatches 48; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                   48; Indels
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/mol_type="genomic DNA"
/strain="CL Brener"
                                                                                      /db xref="taxon:5693"
   Location/Qualifiers
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Matches 41
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TITLE
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/note="Vector: pBS(-) (Stratagene); T. cruzi DNA was
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was gel purified and cloned into the dephosphoryated
Hincli site of the vector"
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Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 366)
Aguero,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.
A random sequencing approach for the analysis of the trypanosoma
cruzi genome: general structure, large gene and repetitive DNA
families, and gene discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Sanchez D.O. Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral San Martin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aires, Argentina, Tel: (54-11) 4980/7255/7
Tel: (54-11) 4752-9639
Email: dsanchez@ilb.unsam.edu.ar
Sequences were basecalled with phred and vector was masked with crossmatch (see http://genome.washington.edu). Sequences were the trimmed from both ends to remove low quality bases and masked
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                                                                          794 GAGTIGACTATCGCCGCCGTCTGGTGTACGAGTCCAGTGACATGGGGA
                                                                                                             421 GAGTTGACCGGCGCGCCGTCTGGTGTACAATTCCGGTGACATGGAGA
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Pred. No. 1.1e-81;
0; Mismatches 15;
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1. .366
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/clone="G43G9"
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Class: shotgun.
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                                                                                                                                                            Ghedin, E., Malek, J., Shetty, J., Khalak, H., Koo, H., Myler, P.,
Stuart, K., Andersson, B. and El-Sayed, N.M.
Greof BAC end sequences from Trypanosoma cruzi CL-Brener TC3
library for gene discovery and map construction
Unpublished (2001)
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Exa: 301 838 0200
Clones are derived from the Trypanosoma cruzi CL-Brener BAC library
TC3. For clone availability, please contact Dr. Bjorn Andersson at
Uppsala University (bjorn.andersson@genpat.uu.se).
Seg primer: M13 For
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Trypanosoma cruzi"
/wol_type="genomic DNA"
/wol_type="genomic DNA"
/wol_type="genomic DNA"
/drom="taxon:5693"
/clone="taxon:5693"
/clone="Tc3-40G16"
/wore="Vector: pBelobaC11; Site_1: Hin dIII; Constructed
for Uppsala University by Marie-Christine Le Paslier in
the laboratory of Denis Le Paslier at the Centre d'Etude
du Polymorphisme Humain (CEPH), Paris, France. Briefly,
Trypanosoma cruzi (L.Brener agarose embedded DNA (obtained
from Dr. Franco da Silveira) was partially digested with
Hin dIII. High molecular weight fragments were ligated in
pBelobaC11 digested with Hin dIII. The average insert
size is 100 kb. Total clone coverage: approx. 33 X the
haploid genome."
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                                                                            Trypanosoma cruzi
Bukaryota; Bujlenosoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1. (bases 1 to 471)
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Pred. No. 1e-86;
0; Mismatches 67;
         BH191346.1 GI:16358622
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Best Local Similarity 85.7%;
Matches 401; Conservative
                                                         Trypanosoma cruzi
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AQ911046
364 bp DNA linear GSS 09-JAN-2001 GSSTC02480 Trypanosoma cruzi random genomic library Trypanosoma cruzi genomic clone G28D17, genomic survey sequence.
                                                                                              Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences were basecalled with phred and vector was masked with crossmatch (see http://genome.washington.edu). Sequences were then trimmed from both ends to remove low quality bases and masked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Euglen.

Eukaryota; Euglen.

Trypanosoma; Schizotrypanum.

1 (bases 1 to 364)

Aguero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.

A random sequencing approach for the analysis of the trypanosoma cruzi genome: general structure, large gene and repetitive DNA families, and gene discovery

Genome Res. 10 (12), 1996-2005 (2000)
                     On Sep 14, 2000 this sequence version replaced gi:9371848. Contact: Sanchez D.O. Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
                                                                      GTGAGGTCACGAAGTCCACTGCGGCGGCAAGATAACTGCGAGTATCAAATGGGGGAGCC
                                                                                                                                                                                                                  TTGGCG--GIGCAGGTGTTGCCATTGTGGCGTCCAACGGGAATCTTGTGTACCCTGTGCA
                                                                                                                                                                                                                                                                                            GGTTACGAACAAAAAGAAGCAAGTTTTTTCCAAGATCTTCTACTCGGAAGACGAGGGCAA
                                                                                                                                                                                                                                                                                                                  241 GGTTACGAACAAAGGAAGCAAGCTCTTCCCAAGATCTTCTACTCGGAAGATGATGGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 364
/organism="Trypanosoma cr
/mol_type="genomic DNA"
/strain="GL-Brener"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: (54-11) 4580/7255/7
Fax: (54-11) 4752-9639
Email: deanchez@iib.unsam.edu.ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Class: shotgun.
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/ organiamonic DNA"

| Lype="genomic DNA"
| /mol type="genomic DNA"
| /mol type="genomic DNA"
| /mol type="genomic DNA"
| /mol type="genomic DNA"
| /db_xxef="weator: pBeloBACI1; Site 1: Hin dIII; Constructed for Uppsala University by Marie-Christine Le Paalier in the laboratory of Denis Le Pasier at the Centre d'Etude du Polymorphisme Humain (CEPH), Paris, France. Briefly, Trypanosoma cruzi CL-Brener agarose embedded DNA (obtained from Dr. Franco da Silveira) was partially digested with Hin dIII. High molecular weight fragments were ligated in pBeloBACI1 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 33 X the haploid genome."
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TC3-53G10.TP TC3 Trypanosoma cruzi genomic clone TC3-53G10, genomic
                                                 240
                                                                                                                                                                     Email: mylerpjøsbri.org
Clones are derived from the Trypanosoma cruzi CL-Brener BAC library
TC3. For clone availability, please contact Dr. Bjorn Andersson at
Uppsala University (bjorn.andersson@genpat.uu.se).
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 367)
Myler, P.J., Aggarwal, G., Fazelinia, G., Mack, J., Marty, A.,
Munden, H. Nelson, S., Pentony, M., Rinta, J., Robertson, L.,
Seyler, A., Sisk, B., Stuart, K., Vogt, C., Worthey, E., El-Sayed, N.M.,
Ghedin, E. and Andersson, B.
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AAGAATTGGGACAGCCACCTGTCCAGCATTTGCACCCCTGCTGATCCAGCCGCTTCGTCG
                   1336 AGTGCCACCAAAACCGAATGGGAGGATGCGTACCGCTGCGTCAACGCAAGCACGCAAAT
                                                                                    TIGICGCAC
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Best Local Similarity 95.6%; Pred. No. 1.5e-78;
Matches 351; Conservative 0; Mismatches 14; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trypanosoma cruzi CL-Brener TC3 BAC-end sequencing Unpublished (2001)
Other GSSs: TC3-53G10.TV
Contact: Peter Wyler
Seattle Biomedical Research Institute
4 Nickerson Street, Seattle, WA 98109, USA
Fax: 206 284 8846
                                                                                                                                                                                                                                                                                                                                                                                                                              BH844382.1 GI:21413850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rypanosoma cruzi
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/note="Vector: pBS(-) (Stratagene); T. cruzi DNA was randomly sheared using a nebulizer and the 1 to 2 Kb range was gel purified and cloned into the dephosphoryated Hincil site of the vector"
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                                                                                                                                                                                                      CGAAGGAATGCGTGTGTGTGTCTTCACACCCGGCTGTTATTTTTAAGGGATGGTGGCTGC
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                                                                                                                                              Gaps
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                                                                                                       Score 315.2; DB 28; Length 364;
Pred. No. 2.3e-74;
0; Mismatches 23; Indels 1;
                                                                                                       Query Match
Best Local Similarity 93.4%;
Matches 340; Conservative
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9, 2004, 00:42:38 Search completed: August Job time: 7678 secs

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241 AGCTACGGCTCATCAAATCCGTGGTGCGTTCCTGGAAGAAGTGGGAACAGCCACCTGTCCA

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 3, 2004, 09:32:50 , Search time 14 Seconds (without alignments) 2488.210 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-086-913-2 3517 1 MGSSHHHHHHSSGLVPRGSH......RAHMGSSSGSSERSTPGSGC 669

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P23253 trypanosoma	_					_	Q59959 streptococc			w	-			_	3 rattus	vibri	рошо	Q9upu3 homo sapien	homo	caen					7	_	_	dict	'n	7 salmonell	4161	P49367 saccharomyc
SUMMARIES	ID	TCNA TRYCR	GP85 TRYCR	8511_TRYCR	NANH_CLOSO	NANH_CLOPE	NANH_SALTY	8513_TRYCR	NANA_STRPN	8512_TRYCR	NANH_CLOSE	NANH BACFR	NANH_MICVI	NANB_STRPN	APU_THETU	NER1_MOUSE	NER1_RAT	NANH_VIBCH	NER1_HUMAN	SOR3_HUMAN	NER2_HUMAN	YS89_CAEEL	WDR1_CAEEL	GUNA_PSEFL	NER2_MOUSE	CAML_FUGRU	DAFT_TRYCR	CBPA_CLOCL	SOR3_MOUSE				- 1	LYS4_YEAST
	Length DB	1162 1	714 1	752 1	404	382 1	381 1	175 1	1035 1	240 1	1014 1	266 1	647 1	697 1	1861 1	409 1	409 1	781 1	415 1	1222 1	380 1	3178 1	611 1	962 1	379 1	1277 1	95 1	1848 1	1219 1	853 1	1159 1	618 1		693 1
4	& Query Match	76.2	23.7	23.2	11.2	11.0	9.8	8.3	•		5.5	•	4.9	4.5	4.2	4.1	4.0	•	•	•	•	3.5		3.4	3.4	3.4	•	•	3.3	•	•	3.5	٠	3.5
	Score	2681	832	815	394.5	388	344	291.5	226.5	208	195	191.5	171.5	157	148.5	142.5	139.5	134	129	125	124.5	122.5	121.5	121	119	118.5	117.5	117.5	116.5	116	114	13.	112.5	112.5
	Result No.		7	e	4	c,	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q88qx8 pseudomonas Q8nr40 corynebacte Q64393 cricetulus Q9z899 chlamydia p Q96gQ0 homo sapien P25391 homo sapien P05421 sus scrofa Q9rxb9 streptomyce Q9y36 pieris bras Q8wy21 homo sapien P74442 synechocyst P35829 lactobacill	
MASZ PSEPK GLGB CORGL PRRZ CRIGR PRP6 CHLPN SORZ HUMAN LMA1 HUMAN LMA1 HUMAN TRIZ STRCO PRSN PIEBR SORI HUMAN Y143 SYNY3 SIAPLACAC	
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725 731 379 1276 1159 3075 3075 1171 850 1161 1191	
112 112 110.5 110.5 110 100.5 1008 1008 1008 1008	
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	

ALIGNMENTS

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Trypanosoma cruzi.
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                       SEQUENCE FROM N.A.
                                                                                               STRAIN=Y;
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     66 MVAIADARYETSNDNSLIDTVAKYSVDDGETWETQIAIKNSRASSVSRVVDPTVIVKGNK 125
                                                                                                                                                         LYVLVGSYNSSRSYWTSHGDARDWDILLAVGEVTKSTAGGKITASIKWGSPVSLKEFFPA 185
                                                                                                                                                                 245
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                                                                                                                                                                                                                                                                      426 SERGCGPAVTTVG----LVGFLSHSATKTEWEDAYRCVNASTANAERVPNGLKFAGVGGG 481
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                                                                                                                                                                                                                                                                                                                                              601
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                                       EMEGMHTNOFLGGAGVAIVASNGNLVYPVQVTNKKKQVFSKIFYSEDEGKTWKFGEGRSD
                                                                                                                                                                                                           PGCSEPVALEWEGKLIINTRVDYRRRLVYESSDMGNSWVEAVGTLSRVWGPSPKSNOPGS
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                                                                                                                       Gaps
                                                                                                                      10;
                                                                                                        Length 1162;
      Pfam; PF02012; BNR, 2.
PRINTS; PR01803; TCSIALIDASE.
Hydrolase; Glycosidase; Glycoprotein; Repeat; GFI-anchor;
                                                                                                                      Indele
                                                                                                      Score 2681; DB 1;
Pred. No. 2.8e-185;
12; Mismatches 50;
                                                                                                                     22; Mismatches
InterPro; IPR008377; Sialidase_trypan.
                                   CYS-RICH
                                                                       342
394
1125
A; 120032 N
                                                                                                       76.2%;
                                                                                                                   Matches 525; Conservative
                                       23 17 163 17 209 22 22 28 58 112 342 394 1125 1125 1162 AA;
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                           Phosphorylation
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Last sequence update) Last annotation update)

GP85 TRYCR STANDARD; PRT, 003877; 01-UN-1994 (Rel. 29, Created) 01-UN-1994 (Rel. 29, Last sequence 10-OCT-2003 (Rel. 42, Last annotati 85 kDa surface antigen precursor.

714 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                     GPI-anchor amidated alanine (Potential).
POLY-ALA.
POLY-THR.
POLY-THR.
BNR 1.
BNR 2.
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PIR; S25216; S35236.
InterPro; IPR0020860; GH BNR.
InterPro; IPR002017; Sialidase_trypan.
Pfam; PF02012; BNR; 2.
PRINTS; PR01803; TCSTALIDASE.
Signal; Multigene family; GPI-anchor; Antigen; Glycoprotein; Repeat; SIGNAL 1. 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                              cruzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
                                  Takle G.B., Cross G.A.M.;
"An 85-kilodalton surface antigen gene family of Trypanosoma crences polypeptides homologous to bacterial neuraminidases.";
Mol. Blochem. Parasitol. 48:185-198 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 23.7%; Score 832; DB 1; Length 71. Local Similarity 33.6%; Pred. No. 3.4e-52; nes 233; Conservative 97; Mismatches 275; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 kDa SURFACE ANTIGEN.
REMOVED IN THE MATURE FORM
(POTENTIAL).
STRAIN=Y;
MEDLINE=92107221; PubMed=1762630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   652
77875 MW;
                                                                                                                          SEQUENCE OF 42-461 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M64836; AAA30150.1; -.
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714
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291
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2268
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171
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714 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285 LSEGISPAKCGAPRITEWEGSLLMIVDCENDQR---VYVSRDMGTTWTEAIGTLSGV-GS 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 AKPFSDVVAGY-IDSAWEWPTLVEKVSESTWOAHTVLGKAEGKKSLDVVLRPTTTKGNK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYVLVGSYNSSRSYWTSHGDARDW-----DILLAVGEVTKSTAGGKITASIKWGSPVS-L 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERVPNGLKFAGVGGGALWPVSQQGQNQRYHFANHAFTLVASVTIHEVPSVASPLLGASLD 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 NESTIAAQKGKUT-EFLASGGSGVVMEDGTIVFSLMAVNEKKOGVFSLIIYSKDNGSTWS 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPKSNQPGSQSSFTA---VTIEGMRVMLFTHPLNFKGRWLRDR-----LNLWLTDNQRIY 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVGQVSIGD--ENSAYSSVLYKDDKLYCLHEINSNEVYSLVFARLVGELRIIKSVLQSWK 406
T.cruzi infection by cleaving sialic acid from cells of the immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSSRVELFKRQSSKVPFEKGGKVTERVVHSFRLPALVNVDGVMVAIADARYETSNDNS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LIDTVAKYSVDDG------ETWETQIAI-KNSRASSVSRVVDPTVIVKGNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 VFLIAGSTDLSYVNWS------WREGSLELKLVVGDVTKPTS-SEPTERIKWGELKSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEFFPAEMEGMHTNQFLGGAGVAIVASNGNLVYPVQVTNKKKQ-VFSKIFYSEDEGKTWK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGEGRSDFGCSEPVALEWEGKL--IINTRVDYRRRLVYESSDMGNSWVEAVGTLSRVWGP
                                    CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in algigosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.

DEVELOPMENTAL STAGE: Mammalian stage of parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Glycosidase; Repeat; Multigene family; Antigen; Signal.
SIGNAL 1 23 POTENTIAL.
                                                                                                                                               MISCELLANBOUS: The parasite mammalian stage surface antigen exhibits extensive antigenic diversity.
SIMILARITY: Belongs to family 33 of glycosyl hydrolases.
SIMILARITY: Contains 2 BNR repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.2%; Score 815; DB 1; Length 752;
Llarity 34.5%; Pred. No. 6.18-51;
Conservative 87; Mismatches 249; Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 752 SIALIDASE 85-1.1.
274 285 BMR 1.
319 330 BMR 2.
752 AA; 80846 MW, BDC33F3EF2DC6859 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
SIALIDASE 85-1.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002860; GH_BNR.
InterPro; IPR008377; Sialidase_trypan.
Pfam; PF02012; BNR; 2.
PRINTS; PR01803; TCSIALIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M62735; AAA30245.1; -. EMBL; X53545; CAA37617.1; -. PIR; A39378; A39378. PIR; S11292; S11292.
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Les 233;
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  LVGSYNSS--RSYWTSHGDARDWDILLLAVGEVTKSTAGGKITASIKWGSPVS-LKEFFPA 185
                                                                                                                                                                                                                                                                                       331 QDSSLHVDALITATIEGRRVMLYTQ----RGNSLGENANPLYLWVTDNNRSFHVGPVGMD 386
                                                                                                                                                                                                                                                                                                                                                    414
                                                                                                                                                                                                                                                                                                                                                                                                446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    447 LSIP-----TAGLVAVLSDAAGDGRWNDBYLCLNATVKNAVKVKDGFQ 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed genes.";
J. Exp. Med. 172:589-597(1900).
-!- FUNCTION: Developmentally regulated neuraminidase implicated in parasite invasion of cells. May contribute to the pathology during
                      161 LAGSSVASNVNGSW-SHGGLK---LKLVVGDVRKPT-DSEQSGRINWGEVQSPLNENSGA
                                                                                    EMEGMHTNOFLGGAGVAI VASNGNLVYPVQVTNKKKQVFSKI FYSEDEGKTWKFGEGRSD
                                                                                                             216 VQERKIT-AFVASGGAGVIMEDGTIVFSIMARNEEEDVYSMIIYSKDDGSTWALSNSVSS
                                                                                                                                                                                                 QSS-----FTAVTIEGMRVMLFTHPLNFKGRWLRDRLN---LWLTDNQRIYNVGQVSI-
                                                                                                                                                                                                                                                                                                                                                                           475 PAGVGGGALWPVSQQGQNQRYHFANHAFTLVASVTIHEVPSVASPLLGASLDSSGGKKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLSYDEKHOWOPIY--GSTPVTPTGSWEMGKRYHVVLTMANKIGSVYIDGEPLEGSGQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPDGRTPDISHFYVGGYGRSDMPTISH --- VTVNNVLLYNRQLNAEBIRTLFLSQDLI--
                                                                                                                                                                          FGCSEPVALEWEGKLI INTRVDYRRRLVYESSDMGNSWVEAVGTLSRVWGPSPKSNQPGS
                                                                                                                                                                                                                                                                                                                                                    -GDENSAYSSVLYKDDKLYCLHEINSNEVYSLVFARLVGELRIIKSVLQSWKNWDSHLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=99324879; PubMed=1695668;
Kahn S., van Voorhis W., Eisen H.;
"The major 85-kD surface antigen of the mammalian form of Trypanosoma
cruzi is encoded by a large heterogeneous family of simultaneously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Тгураповоща
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MEDLINE=91239592, PubMed=2034687;
Kahn S., Colbert T.G., Wallace J.C., Hoagland N.A., Eisen
"The major 85-kDa surface antigen of the mammalian-stage f
"The major antigen of the mammalian-stage f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trypanosoma cruzi.
Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Last sequence update)
28-FRB2-2003 (Rel. 41, Last annotation update)
Sialidase 85-1.1 precursor (EC 3.2.1.18) (Neuraminidase)
85 kDa surface antigen) (SA85-1.1 protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trypanosoma cruzi is a family of sialidases.";
Proc. Natl. Acad. Sci. U.S.A. 88:4481-4485(1991).
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P18269;
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23;

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CLOPE
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              SEQUENCE
                                          Query Match
Best Local 8
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500 TKVKDGFQLTEPDSRAVWSVNIPDGNVRHISLSHNFTLVASVIIEEAPSGNTPLLTAVLV 559
                                                                      619
                                                                                                     625
                                                                                                                                   668
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                                                         560 DAGPEYFMRLSYTADNKWMTMLKDEKKPTTESRPWEAGKEHQVALMLQGNKASVYVDGEL
                               SSGGKKLLGLSYDEKHQWQPIY--GSTPVTPTGSWEMGKRYHVVLTMANKIGSVYIDGEP
                                                                                            LEGSGQTVVP-------DGRTPDISHFYVGGYGRSDMPTISHVTVNNV
                                                                                                                         L---GEBEVPLTGEKPLEIFAFCFGACKIDGDEESSPKEIGKKPR-----VTVTNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gen. Microbiol. 135:3087-3096(1989).
- FUNCTION: SIALIDASES HAVE BEEN SUGGESTED TO BE PATHOGENIC FACTORS IN MICROBIAL INFECTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1 - CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal stalic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
-1 - SUBCELLULAR LOCATION: Periplasmic.
-1 - PTW: IT IS POSSIBLE THAT THE SIALIDASE IS CLEAVED IN FRONT OF A CYSTEINE WHITHIN THE LEADER PEPTIDE, FORMING A GLYCERIDE THIOETHER BOND WHICH LINKS THE PROTEIN TO THE MEMBRANE. A SECOND PROTEOLYTIC CLEAVAGE RELEASES THE MATURE EXTRACELLULAR FROTEIN.
-1 - SIMILARITY: Belongs to family 33 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rothe B., Roggentin P., Frank R., Bloecker H., Schauer R.; "Cloning, sequencing and expression of a sialidase gene from Clostridium sordellii G12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO1803; TCSIALIDASE.
PROSITE; PS00013; PROKAR LIPOPROTEIN; UNKNOWN 1.
Hydrolage; Glycosidase; Periplasmic; Signal; Repeat.
                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sialidase precursor (EC 3.2.1.18) (Neuraminidase).
                                                                                                                                                                                                                                                                       404 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       [1] SEQUENCE FROM N.A., AND SEQUENCE OF 28-45.
STRAIN=ATCC 9714 / NCIB 10717;
MEDLINE=90132537; Pubmed=2693593;
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InterPro; IPR002860; GH BNR.
InterPro; IPR000437; Prok lipoprot_S.
InterPro; IPR008377; Sialidase_trypan.
Pfam; PF02012; BNR; 5.
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BNR 3.
BNR 4.
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                                                                                                                                                        626 LLYNRQLNAEEIRTL 640
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669 FLYNRPLNSTEMRAI 683
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284
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P15698;
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ACTAINS-899;
AN REDLINE-89005674; PubMed=2901987;
RA ROGGERIA P., Rothe B., Lottepeich F., Schauer R.;
RAGGERIA R., Rothe B., Lottepeich F., Schauer R.;
RAGGERIA R., Rothe B., Lottepeich F., Schauer R.;
RT "Cloning and sequencing of a Clostridium perfringens sialidase gene.",
RT "Cloning and sequencing of a Clostridium perfringens sialidase gene.",
RT FEBS Lett. 238:31-34(1988).
- FEBS Lett. 238:31-34(1988).
- TOTAINS SINTERPROPERIONS.
- C CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->8)-4 phycosidic linkages of terminal sialic residues in alpha-(2--8)-9lycoproteins, glycolipids, colominic acid and synchetic substrates.
- C SIMCLARITY: Belongs to family 33 of glycosyl hydrolases.
- SIMILARITY: Contains 4 BNR repeats.
- C - SIMILARITY: Contains 4 BNR repeats.
- C - DATABASE: NAME=Worthington enzyme manual;
- C - DATABASE: NAME=Worthington enzyme manual;
                                                                                                                                                   SRVVDPTVIVKG-NKLYVLVGSYNSSRSYWTSHGDAR-DWDILLAVGEVTKSTAGGKITA 169
                                                                                                                                                                                                                                                                    166
                                                                                                                                                                                                                                                                                                                                                                                                                                       282
                                                                                                                                                                                                                                                                                               170 SIKWGSPVSLKEFFPAEMEGMHTNQ--FLGGAGVAIVASNGNLVYPVQVT---NKKKQVF 224
                                                                                                                                                                                                                                                                                                                                                                                              283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 VEAVGILSRVWGP----SPKSNQPGSQSSFTAVII-EGMRVMLFTHPLNFKGRWLRDRLN 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 ------EVYDPLHNKISTGNGSGCQGSFIKVTAKDGHRLGFISAPKNTKGGYVRDNIT 334
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                                                                                                                          54 FRLPALVNV-DGVMVALADARYETSNDNSLIDTVAKYSVDDGETWETQIAIKNSRA-SSV
                                                                                                                                                                                                                                      |||:| | :| :::||:| :::|
SRVMDSTTVVTDTGRIILIAGSWNKNGNWASSTTSLRSDWSVQMVYSDDNGET-----
                                                                                                                                                                                                                                                                                                                        ---WSDKVDLT-NKARIKNQPSNTIGWLAGVGSGIVWSDGTIVMPIQIALRENNANNYY
                                                                                                                                                                                                                                                                                                                                                                                225 SKIFYSEDEGKTWKFGEGRSDFGCSEPVALEWEGKLIINTRVDYRR-RLVYBSSDMGNSW
                                                                                                                                                                                                                                                                                                                                                                                                              Gaрв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 VYMIDFDDLSKGIRELCSPYPEDGNSSGGGYSCLSFNDGKLSILYEANGNIEY 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1502;
                                                                                          41,
                                               Length 404;
                                                                                        Indels
  525B9DA90083AA6A CRC64;
                               11.2%; Score . 5.4e--...
30.9%; Pred. No. 5.4e--...
**ve 67; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Sialidase (EC 3.2.1.18) (Neuraminidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 AA
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  44729 MW;
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                                                             al Similarity 30.9
109, Conservative
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404 AA;
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REPEAT
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 16;
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                                                                                                                                                                                                                111 VSRVVD-PTVIVKGNKLYVLVGSYNSSRSY-WTSHGDARDWDILLAVGEVTKSTAGGKIT 168
                                                                                                                                                                                                                              95 YSRVMDSTTVITNTGRILLIAGSWNTNGNWAMTTSTRRSDWSVQMIYSD-----D 144
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                                                                                                                                                                                                                                                                                                     225 SKIFYSEDEGKTWKFGEGRSDFGCSEPVALEWEGKLIINTRVDYR-RRLVYESSDMGNSW 283
                                                                                                                                                                                                                                                                                                                                              284 VEAVGILSRVWGPSPKSNQPGSQSSF-TAVTIEGMRVMLFTHPLNFKGRWLRDRLNLWLT 342
                                                                                                                                                                                                                                                                                                                                                          -EIYEPLN---GKILTGKGSGCQGSFIKATTSNGHRIGLISAPKNTKGEYIRDNIAVYMI 320
                                                                                                                                                                                    36 FRIPNIQLIN-DGTILTFSDIRYNGPDDHAYIDIASARSTDFGKTWSYNIAMKNNRIDST 94
                                                                                                                                                                                                                                                                                                                                                                                                   D-NQRIYNVGQVSI-----GDE-NSAYSSVLYKDDKLYCLHEINSN-----EVYSLV 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nayyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.,
                                                                                                                                                                                                                                                           169 ASIKWGSPVSL-KEPFPAEMEGMHTNQFLGGAGVAIVASNGNLVYPVQVT---NKKKQVF
                                                                                                                                                                                                                                                                       SLIIYSKDNGETWTMGNKVPNSNTSENWVIELDGALIMSTRYDYSGYRAAYISHDLGTTW
                                                                                                                                                    40; Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sialidase (EC 3.2.1.18) (Neuraminidase) (N-acylneuraminate glycobydrolase) (STNA).
NANH OR STM0928.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92292952; PubMed=1602967;
Hoyer L.L., Hamilton A.C., Steenbergen S.M., Vimr E.R.;
"Cloning, sequencing and distribution of the Salmonella typhimurium
LT2 sialidase gene, nanH, provides evidence for interspecies gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                                                                                                                           11.0%; Score 388; DB 1; Length 382; 30.4%; Pred. No. 1.5e-20; ive 72; Mismatches 138; Indels '
                                                                                                         D50857BB50A4E886 CRC64;
HSSP; P29768; 2SIL.
InterPro; IPR002860; GH BNR.
InterPro; IPR00817; Sialidase_trypan.
Pfam; PF02012; BNR; 4.
PRINTS; PR01803; TCSIALIDASE.
Hydrolase; Glycosidase; Periplasmic; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   381 AA
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STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                    BNR 3.
BNR 4.
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                                                                                                         382 AA; 42813 MW;
                                                                                                                           Query Match
Best Local Similarity 30.4%,
Matches 109; Conservative
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208
255
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Sheldrick G.M.;
Submitted (JUL-1998) to the PDB data bank.
Submitted (JUL-1998) to the PDB data bank.
I- FUNCTION: CLEAVES THE TERMINAL STALIC ACID (N-ACETYL NEURAMINIC ACID FOR CALD WHICH CAN BE USED AS CARBON AND ENERGY SOURCES.
STALIC ACID WHICH CAN BE USED AS CARBON AND ENERGY SOURCES.
SIALIC ACID WHICH CAN BE USED AS CARBON AND ENERGY SOURCES.
SIALIC ACID WITH: HYDROLYSIS OF BATHOGENIC FACTORS IN MICROBIAL INFECTIONS.
-!- CATALYNTY: Hydrolysis of alpha-(2->8)-4, alpha-(2->6)-4, alpha-(2->8)-4) alpha-(2->9)-4) alpha-(2->9)-4) alpha-(2->6)-4, alpha-(2->6)-4, alpha-(2->6)-4) alpha-
Complete genome sequence of Salmonella enterica serovar Typhimurium
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MEDINE=96228252; PubMed=8656428;
MEDINE=96228252; PubMed=8656428;
Crennell S.J., Garman B.F., Philippon C., Vasella A., Laver W.G., Vimr E.R., Taylor G.L.;
Vimr E.R., Taylor G.L.;
"The structures of Salmonella typhimurium LT2 neuraminidase and its complexes with three inhibitors at high resolution.";
J. Mol. Biol. 259:264-280(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND REVISIONS TO C-TERMINUS
                                                                                                                                                                                                                                                                                                                                    MEDLINE-92389334; PubMed=1518058;
Taylor G.L., Vinr B.R., Garman B.F., Laver W.G.;
"Purification, crystallization"
"Purification, crystallization of preliminary crystallographic e
of neuraminidase from Vibrio cholerae and Salmonella typhimurium
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StyGene; SG10244; nanH.
InterPro; IPR003860; GH BNR.
InterPro; IPR003377; Sialidase_trypan.
Pfam; PF02012; BNR; 4.
PRINTS; PR01803; TCSIALIDASE.
Glycosidase; Hydrolase; Repeat; 3D-structure; Complete proteome.
INIT_MET
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Crennell S.J., Garman B.F., Laver W.G., Vimr B.R., Taylor G.L.;
"Crystal structure of abacterial sialidase (from Salmonella
typhimurium LT2) shows the same fold as an influenza virus

    -i- SÜBÜNIT: Monomer.
    -i- SIMILARITY: Belongs to family 33 of glycosyl hydrolases.
    -i- SIMILARITY: Contains 4 BNR repeats.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuraminidase.";
Proc. Natl. Acad. Sci. U.S.A. 90:9852-9856(1993)
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                                                                                                                   Nature 413:852-856(2001)
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TVAKYSVDDGETWETQIAIKNSRASS-VSRVVDPTVIVKG----NKLYVLVGSYNSSRSY 139
                                                                    WTSHGDA---RDWDILLAVGEVTKSTAGG----KITASI-----KWGSPVSLKEFFPAEM 187
                                                                                                                        ---ISAMLGGVGSGLQLNDGKLVFPVQMVRTKNITTVLNTSPIXSTDGITWSLPSGYCE 225
                                                                                                                                         246 FGCSEPVALEWEGKLIINTRVDYRRRLVYESSDMGNSWVEAVGTLSRVWGPSPK---SNQ 302
                                                                                                                                                   PGSQSSFTAVTIEGMRVMLFTHPLNFKGRWLRDRLNLWLTDNQRIYNVGQVSIGDE--- 358
                                                                                                                                                                                       277 HGVQGSTITIPSGNKLVAAHSSAQNKANDYTRSDISLYA---HNLYS-GEVKLIDDFYPK 332
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        EGMHTNQFLGGAGVAIVASNGNLVYPVQVTNKKK--QVFSKIFYSEDEGKTWKFGEGRSD
                                                                               expressed genes.", J. 539-597(1990).
J. BXP. Med. 172:589-597(1990).
-I- FUNCTION: Developmentally regulated neuraminidase implicated in parasite invasion of cells. May contribute to the pathology during T.cruzi infection by cleaving stalic acid from cells of the immune
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CL;
MEDLINE=90324879; PubMed=1695668;
Kahn S., van Voorhis W., Eisen H.;
"The major 85-kD surface antigen of the mammalian form of Trypanosoma cruzi is encoded by a large heterogeneous family of simultaneously
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!-GATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal stalic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
-!- DEVELOPMENTAL STAGE: Mammalian stage of parasite.
-!- MISCELLANEOUS: The parasite mammalian stage surface antigen exhibits extensive antigenic diversity.
                                                                                                                                                                                                                                                                                          (Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 41, Last annotation update)
5-1.3 (EC 3.21.18) (Neuraminidaee) (NA) (Wajor 85 kDa igen) (SA85-1.3 protein) (Fragment).
                                                                                                                                                                                                              ----NSAYSSVLYK----DDKLYCLHEINSNEVYSLVFARLVGELRIIKS 400
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surface antigen)
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28-FEB-2003
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28.2%; Pred. No. 2.2e-17;
iive 63; Mismatches 154; Indels
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                                              -> A (IN REF. 1).
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Best Local Similarity 28.2<sup>1</sup>
Matches 116; Conservative
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381 AA;
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EMBL; X53547; CAA37619.1; -. PIR; S11294; S11294.

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                                                                                                                                                                                                                                                        576 GSVYIDGEPLEGSGQTVVP-DGRTP-DISHFYVGGYGRSDMPTISHVTVNNVLLYNR 630
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MEDLINE-21429245; PubMed=11544234;

Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., Berrem S.T., Fritz L., Pu D.-J., Fuller W., Geringer C., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Morris P.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R., Jr., Skatrud P.L.,
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MEDIATESCOCYPE 6;
MEDIATESCOCIANG PUBMED=875848;
MEDIATESCOCIANG PUBMED=875848;
MEDIATESCOCIANG PUBMED=875848;
MEDIATESCOCIANG PUBMED A.C.;
PCIONING and characterization of nanB, a second Streptococcus
pneumoniae neuraminidase gene, and purification of the NanB enzyme
from recombinant Escherichia coli.";
J. Bacteriol. 178-4854-4860(1996).
-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal simic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
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                                                                                  8.3%; Score 291.5; DB 1; Length 175;
                PRINTS; PR01803; TCSIALIDASE. —
Hydrolase; Glycosidase; Repeat; Multigene family; Antigen.
                                                                                                              75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                      175 AA; 19552 MW; E90DD13274B75B8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                     Q59959; Q54722;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sialidase A precursor (EC 3.2.1.18) (Neuraminidase A)
NANA OR SPR1536.
                                                                                               ; Pred. No. 4.3e-14; 26; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                           PRT; 1035 AA.
InterPro; IPR008377; Sialidase_trypan.
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                                                                         Query Match
Best Local Similarity 39.0%;
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InterPro; IPR003985; ConA_like_lec_gl.

InterPro; IPR003695; GH_BUR.

InterPro; IPR003697; GF_BUR.

InterPro; IPR0036977; Gpos_YSIR.

InterPro; IPR0036977; Gpos_YSIR.

InterPro; IPR0036977; Gpos_YSIR.

InterPro; IPR00399; Gram_pos_anchor.

InterPro; IPR00399; Gram_pos_anchor.

InterPro; IPR00399; SIRIR.

InterPro; IPR00391; Indinin_G.

INTERPAMS; IIGR01167; IPXTG anchor; I.

INTERPAMS; IIGR01167; IPXTG anchor; I.

INTERPAMS; IIGR01168; VSIRK_signal; I.
SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIALIDASE A.

REMOVED BY SORTASE (POTENTIAL).

LEXTG SORTING SIGNAL (POTENTIAL).

LEXTG SORTING SIGNAL (POTENTIAL).

114741 MW; C588A2D7A12E12F3 CRC64;
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                                  an amide bond (Potential).
SIMILARITY: Belongs to family 33 of glycosyl hydrolases.
SIMILARITY: Contains 4 BNR repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE008522; AAL00340.1; -. EMBL; U43526; AAC44391.1; -. PIR; 989063; 989063. PIR; 730287; T30287. HSSP; Q02834; 1EUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WTSHGDARDWDILL -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CI;

MEDLINE=90324879; PubMed=1695668;

Kahn S., van Voorhis W., Elsen H.;

The major 85-kb surface antigen of the mammalian form of Trypanosoma cruzi is encoded by a large heterogeneous family of simultaneously expressed genes.";

J. Exp. Med. 172:589-597 (1990).

-!- FUNCTION: Developmentally regulated neuraminidase implicated in parasite invasion of cells. May contribute to the pathology during T.cruzi infection by cleaving sialic acid from cells of the immune
312 VIIEGMRVMLFTH---PLNFKGRWLRDRLN----LWLTDN-----QRIYNVGQVSIGDE
                        703 TMHEGKEYIILSNAGGPKRENGMYHLARVEENGELTWLKHNPIQKGEFAXN----SLQEL
                                                               359 NSAYSSVLYKDDKLYCLHEINSNEVYSLVFARLVGELRIIKSVLQSWKNWDSHLSSICTP
                                                                                                                                419 ADPAASSSERGCGPAVTTVGLVGFLSHSATKTEWEDAYRCVNASTA------N
                                                                                                                                                                797 TE-AKVKRTREMGK----GVIGLEFDSEVLVNKAPTLQLANGKTARFMIQYDTKTLLFT
                                                                                                                                                                                                 466 AERVPNGLKFAGVGGAL----WPVS-----QQGQNQRYHFANHAFTLVASVTIHEVP
                                                                                                                                                                                                                                 851 VDSEDMGQKVTGLAEGAIESMHNLPVSVAGTKLSNGMNG------SEAAVHEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal stalic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-Sepres-2003 (Rel. 41, Last annotation update)
Sialidase 85-1.2 (EC 3.2.1.18) (Neuraminidase) (NA) (Major 85 kDa Surface antigen) (SA85-1.2 protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR008377; Stalidase_trypan.
PRINTS; PR01803; TCSIALIDASE.
Hydrolase; Glycosidase; Repeat; Multigene family; Antigen.
                                                                                                                                                                                                                                                                                                                                                                                            240 AA.
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P18270;
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5.9%; Score 208; DB 1; Length 240;

26600 MW; 8B73A9F7EE19ED9C CRC64;

240 AA;

NON TER SEQUENCE Query Match

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                                                       490 GONORYHFANHAFTLVASVTIHEVPSVASPLLGASLDSSGGKKLLGLSYDBKHOWQPIYG 549
                                                                                                                                                                    64 GDKKLTTESRPWVPKKEHQVALMLQGNKASVYIDGESLGEEAPLTVETPLEPFGFCFGAC 123
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                                                                                                                                                                                                                                                    124 DFDDDDGGDDDDEBDSQEESSPKESSPE-----KIGKK-----PHVIVINVFLYNRP 171
                                                                                586 ------EGSGQTVVPDGRTPDISHFYVGGYGRSDMPTISHYTVNNVLLYNRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=NC 0054714;
MEDLINE-91238693; PubMed-2034213;
Rothe B., Rothe B., Roggentin P., Schauer R.;
Rothe B., Rothe B., Roggentin P., Schauer R.;
The sialidase gene from Clostridium septicum: cloning, sequencing, expression in Escherichia coll and identification of conserved sequences in slalidases and other proteins.";
Mol. Gen. Genet. 226:190-197(1991)
--- FUNCTION: SIALIDASES HAVE BEEN SUGGESTED TO BE PATHOGENIC FACTORS IN MICROBIAL INFECTIONS.
                                  Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- CATALTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
-1- SUMCELLULAR LOCATION: Periplasmic.
-1- SIMILARITY: Belongs to family 33 of glycosyl hydrolases.
-1- SIMILARITY: Contains 4 BNR repeats.
-1- SIMILARITY: Contains 1 F5/8 type C domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium septicum.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                              503
      Pred. No. 7.2e-08;
5; Mismatches 63; Indels
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R InterPro; IPR008985; ConA_like_lec_gl.
R InterPro; IPR008979; Gal_Eind_like.
R InterPro; IPR008979; Gal_Eind_like.
R InterPro; IPR008160; GH_ENR.
R InterPro; IPR008160; GH_ENR.
R InterPro; IPR008160; GH_ENR.
R PR02973; Bialidase N; 1.
PR081TE; PS50022; FA58C_3; 1.
Hydrolase; Glycosidase; Periplasmic; Signal; Repeat.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Sialidase precursor (EC 3.2.1.18) (Neuraminidase).
                                                                                                                                   550 STPVTPIGS--WEMGKRYHVVLTMANKIGSVYIDGEPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1014 AA
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  ilarity 32.3%; Pre
Conservative 15;
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Best Local Similarity
Matches 61; Conserv
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                      61;
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P29767;
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Bacteroides fragilis
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                                          NCBI_TaxID=817;
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                                                                                                                                             391 GSNNFRIPALYTTKDGTVLASIDVRKGGGHDAPNNIDTGIKRSTDGGVTWDEGKIILDYP 450
                                                                                                                                                                                                                      ----SRVVDPTVIVKGNKLYVLVGSYNSSR 137
                                                                                                                                                                                                                                                                171
                                                                                                                                                                                                                                                                                                          KWGSPVSLKEPFPAEMEGMHTNQFLG---GAGVALVASN--GNLVYPVQVTNKKKQVFSK 226
                                                                                                                                                                                                                                                                                                                                                     286
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                                                                                                                                                                                                                                                                                                                                                                                                                     ITT-----NTSGCVGQLTECQVVEMP------NGQLKMFMRNTGG 692
                                                                                                                                                                                                                                                                                                                                                                                                                                            347 IYNVGQVSIG---DENSAYSSVLYKDDKL---YC-LHEINSNEVYSLVFARLVGELRIIK 399
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                                                                                                                                                                                                                                                                                                                       571 TWSDPIDLAKKEVKTDW-----MRFLGTGPGKGHQIKTGRYAGRLLFPVYLTNASGFQSSA
                                                                                                                                                                                                                                                                                                                                                     I PYSEDECKTWKFGEGRSDFGCSEPVALEWEGKLI INTRVDYRRRLVYESSDMGNSWVEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 824 DYLKADLLQDVPAANIKSYTTNSENNIYDPGDKISLNVTFD---QTVSLIGDRTITA---
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                                                                                                                             PRGSHMAPGSSRVELF-------KRQSSKVPFEKGGKVTERV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLKIVN---VVNKVIDITEDRNIGLAVQVGEEVQSVDKTILLQDLVDSTSNL 968
                                                                                  5%; Score 195; DB 1; Length 1014; O%; Pred. No. 5e-06; Indels 264;
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                             BNR 2.
BNR 3.
BNR 4.
MW; C4F49233473A2FAD CRC64;
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ID MANH BACFR
CONTROL OF THE STANDARD; PRT; 266 AA.

AC P31206;
DT 01-UUL-1993 (Rel. 26, Created)
DT 01-UUL-1993 (Rel. 26, Last sequence update)
DT 28-FFB-2003 (Rel. 41, Last annotation update)
DT Salidase (EC 3.2.1.18) (Neuraminidase) (Fragment).
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          TYPE
 SIALIDASE
                                                                                                          Conservative 117;
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20.0%;
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                      442
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638
711
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                     431
563
627
700
                                                                                                           Matches 154;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 LOGPGRGITMSDGTLVFPTQFIDSTRVPNAGIMYSKDGGKNWKMHNYARTNTTBAQVAEA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEGKLIINTRVDYR--RRLVYESSDMGNSWVEAVGTLSRVWGPSPKSNQPGSQSSFTAVT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuraminidase gene, nanH, in Bscherichia coli.";
J. Bacteriol. 172:2594-2600(1990).
-!- FUNCTION: SIALIDARES HAVE BEEN SUGGESTED TO BE PATHOGENIC FACTORS IN MICROBIAL INFECTIONS.
-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STDGGKTWEKMRLPLAFGEFGGLPAGQNGVGDPSILVDTKTNNVWVVAAWTHGMGNQRAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGGAGVAIVASNGNLVYPVQVTNKKKQVFSKIFYSEDEGKTWKFGEGRSDFGCSEPVALE
                                                                                                                                                                                                                                                                                                                                                   alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic subtrates.
SUBCELLULAR LOCATION: Periplasmic.
SIMILARITY: Belongs to family 33 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47;
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
                                                                                                                                          STRAIN=TAL2480;
MEDILINE=902592; PubMed=2158974;
KBUSG T.A. Thompson J.S., Godoy V.G., Malamy M.H.;
"Cloning and expression of the Bacteroides fragilis TAL2480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  647
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InterPro; IPR008377; Sialidase_trypan.
Pfam; PF02012; BNR; 5.
PRINTS; PR01803; TCSIALIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 44 4
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BNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69; Conservative
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95
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266
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ID NANH MICVI
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us-10-086-913-2.803.rsp

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                                                                                                                                                                                                                                                 X.FAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).

X.FAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).

X. MEDLINE=96164436; Pubmed=8591030;

ABBLINE=96164436; Pubmed=8591030;

AGBREAL A., Crenell S., Taylor G.;

AGBREAL A., Crenell S., Taylor G.;

Immunoglobulin module and a galactose-binding jelly-roll.";

Structure 3:1197-1205 (1995).

STROGYION: TO RELEASE SIALIC ACIDS FOR USE AS CARBON AND EATHOGENIC MICROORANISMS, SIALIDASES HAVE BEEN SUGGESTED TO BE PATHOGENIC FACTORS.

C. I. FUNCTION: TO RELEASE SIALIC ACIDS FOR THIS NON-PATHOGENIC BACTERIUM WHILE IN PATHOGENIC PACTORS.

C. I. FUNCTION: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->9)-, alpha-(2->9)-,
                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 38-647.
STRAIN-ATCC 31146;
SARAIN-ATCC 31146;
SAKURADA K., Ohta T., Hasegawa M.;
Cloning, expression, and characterization of the Micromonospora viridifaciens neuraminidase gene in Streptomyces lividans.";
J. Bacteriol. 174:6896-6903(1992).
                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micromonosporineae; Micromonosporaceae; Micromonospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACID.
-1- SIMILARITY: Belongs to family 33 of glycosyl hydrolases.
-1- SIMILARITY: Contains 5 BNR repeats.
-1- SIMILARITY: Contains 1 F5/8 type C domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jensen

Jeroffermat

Jensen

J
            01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Sialidase precursor (EC 3.2.1.18) (Neuraminidase).
                                                                                Micromonospora viridifaciens
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                                                                                                                                                                                                                                                                                                                                      MEDLINE=21357209; PubMed=11463916;
MEDLINE=21357209; PubMed=11463916;
MEDLINE=21357209; PubMed=11463916;
Peterlin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D..,
Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey B.K.,
Holt I.E., Löftus B.J., Yang F., Smith H.O., Venter J.C.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
"Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----KUPFE---KGGKVTERWHSFRLPALVNV-DGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 293:498-506(2001).
--- CATALYTIC ACTIVITY: Hydrolygis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->6)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
--- SIMILARITY: Belongs to family 33 of glycosyl hydrolases.
--- SIMILARITY: Contains 4 BNR repeats.
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                                                                                                                                                                                   STRAIN=Serotype 6;
MEDLINE=96326329; PubMed=8759848;
BERY A.M., Lock R.A., Paton J.C.;
"Cloning and characterization of nanB, a second Streptococcus pneumoniae neuraminidase gene, and purification of the NanB enzyme from recombinant Escherichia coli.";
J. Bacteriol. 178:4854-4860(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167; Indels 180;
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InterPro; IPR002860; GH_BNR.
InterPro; IPR002860; GH_GNZ.
Fam; PF02012; BNR, 4.
Pfam; PF02012; Sialidase N; 1.
Hydrolase; Glycosidase; Repeat; Signal; Complete proteome.
SIGNAL
                                                                                                  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                 â
               16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sialidase B precursor (EC 3.2.1.18) (Neuraminidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K -> B (IN REF. 1).
D -> G (IN REF. 1).
T -> N (IN REF. 1).
N -> D (IN REF. 1).
K -> R (IN REF. 1).
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TIGR; SP1687; -.
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   Created)
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                                                                                      Streptococcus pneumoniae
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222
393
639
697 AA;
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 (Rel.
(Rel.
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           FROM N.A.
                                                                                                                                       NCBI_TaxID=1313;
                                                                   NAMB OR SP1687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae.";
                                                                                                                       Streptococcus
15-DEC-1998
16-OCT-2001
28-FEB-2003
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 YNSSRSYWTSHG------DARDWDILLAVGEVTKSTAGG-----KITASIK----WG 174
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                                                                                                                                                                                                                                                                                                                                             GSHMAPGSSRVELFKRQSSKVPFEKGGKVTERVVHSFRLPAL-VNVDGVMVAIADAR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 IFNFHVYSQRQGFAGSRPGTDPADPNVLHA--NVATSTDGGLTWSHRTITADITPDPGWR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVWGPSPKSNQ-----PGSQSSFTAVTIEGMRVMLFTHPLNFKGRWLRDRLNLWLTDNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDL.-PDPTNNASIIRAFPDAPAGSARA----KVLLPSNAASQTSR-SQGTIRMSCDDGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 TWPVSKVFQPGSMS----YSTLTALPDGTYGLLYEPGTGIRYA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395 NFNLAW-----LGGICAPFTIPDVALEPGQQVTVPVAVTNQSGIAVPKPSLQLDASPDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                511 HEVPSVASP---LLGASLDSSGGKKLLGLSYDEKHQWQPIYGSTPVTPTGSWEMGKRYHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 568 VLIMANKIGSVYIDGEPLEGSGQTVVPDGRTPDI----SHFYVGGYGRSDMPTISH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLLDQARMSIADVDSE-----ETAREDGRASNVIDGNPSTFWHTEWSRADAPGYPHRIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVLOSWKNWDSHLSSICTP---ADPAASSSERGCGP-AVTTVGLVGFLSHSA---TKTEW
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                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                        4.9%; Score 171.5; DB 1; Length 647; 21.9%; Pred. No. 0.00013; Live 93; Mismatches 241; Indels 211;
                                                                                                                                                                                                                                        68830 MW; DCC1FE5BC935B8AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----VIVNNVLLYNRQLNA--EEIRTLFLSQDLIGT
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                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                      602
626
639
638
                                                                                                                                                                                                                                        647 AA;
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
 526
533
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NANB_STRPN
ID NANB_STRPN
AC Q54727;
                                                                                                                                                                                                                                                                                            Best Local Sim:
Matches 153;
                                                                                                                                                                                                                       STRAND
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199 YLAKGSIDEISLFNKAISDQEVSTIPLSNPFQLIFQSGDSTQ--ANYFRIPTLYTLSSGR 256
                                               SRASSVSRVVDPTVI -- VKGNKLYVL-----VGSYNSSRS-----YWTSHGDA 146
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STEALULE FACUATION N.A.

MEDINE-94252999; PubMed-8195085;

Matuschek M., Burchhardt G., Sahm K., Bahl H.;

Matuschek M., Burchhardt G., Sahm K., Bahl H.;

Matuschek M., Burchhardt G., Sahm K., Bahl H.;

"Pullulanase of Thermonaerobacterium thermosulfurigenes EMI
"Clostridium thermosulfurogenes): molecular analysis of the gene,

"Composite structure of the enzyme, and a common model for its

"Composite structure of the enzyme, and a common model for its

"ATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
"Inkages in oligosaccharides and polysaccharides."

"Inkages in pullulan and in amylopectin and glycogen.

"Composite of the composite of the enzyme."

"Inkages in oligosaccharides and polysaccharides."

"Inkages in pullulan and in amylopectin and glycogen.

"Alpha and beta-limit dextrins of amylopectin and the alpha and beta-limit dextrins of subunit (By similarity).

"Inkages in Calcium ion per subunit (By similarity).

"Inkages in Calcium ion per subunit (By similarity).
                                                                                                                                                                                                                                                                           377 GÖNDFRYTVRENGVVYNETTNKPİNYTINDKYEVLEGGKSLIVEQYSVDFDSGSLRERHN
                                                                                                                                                                                                 GSPVSLKEFF-----PAEMEGMHTNQ------FLG-----GAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Amylopullulanase precursor (Alpha-amylase/pullulanase) (Pullulanase
type II) [Includes: Alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase); Pullulanase (EC 3.2.1.41) (1,4-alpha-D-glucan
glucanohydrolase) (Alpha-dextrin endo-1,6-alpha-glucosidase)].
                                                                                                                                                                                                                                                                                                                                                                                                                         365 VLYKDDKLYCLHEINSNEVYSLVFARLVGELRIIKSVLQSWKNWDSHLSSI 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                 636 IDWKYH--YDIDLPSYGYAYSAITELPNHHIGVLFEKYDSWSRNELHLSNV 684
                                                                                                                                          RDWDILLAVGE-----VTKST------AGGKITASIKW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to family 13 of glycosyl hydrolases. SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales, Thermoanaerobacteriaceae, Thermoanaerobacterium.
                             MVAIADARYETSNDN-SLIDTVAKYSVDDGETWETQI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermoanaerobacter thermosulfurogenes (Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 YETSNDNSLIDTVAKYSV----DDGETWETQIAIKNSRASSVSRVVDPTVIVKGNKLYVL 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 GAGVAIVASNG-NLVYPVQVTNKKKQVFSKIFYSEDEGKTWKFGEGRSDFGCSEPVAL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----EWEGKLIINTRVDYRRRLVYESSDMGNSWVEAVGTLSRVWGPS------PKS
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CALCIUM (VIA CARBONYL OXYGEN) (B
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CALCIUM (BY SIMILARITY).
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PROSITE; PS01072; SLH DOWAIN; 3.
Carbohydrate metabolism; Multifunctional enzyme; Hydrolase; Glycosidase; Calcium-binding; Repeat; Signal; Glycoprotein. SIGNAL
Contains 3 S-layer homology (SLH) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         453 453 CALCIUM (BY SIMILARITY).

1681 1739 SIH 1.

1740 1803 SIH 2.

1804 1861 SIH 3.

1734 1734 D -> E (IN REF. 1; AABOO841).

1861 AA; 206104 MW; 06C23070B453B574 CRC64;
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FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
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Pred. No. 0.027;
97; Mismatches 234;
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                                                                                                                                                                                                                                                           InterPro; IPR006589; Alp amyl_cat_sub. InterPro; IPR006048; Alpha_amyl_c. InterPro; IPR006049; Alpha_amyl_cat. InterPro; IPR001961; FV_III. InterPro; IPR00196185; Glyco_hydro_131G. InterPro; IPR004185; Glyco_hydro_131G. InterPro; IPR004193; Glyco_hydro_131G. InterPro; IPR004193; Glyco_hydro_131N. InterPro; IPR001119; SLH.
                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; Pr00128; alpha-amylase; 1.
Pfam; Pr02806; alpha-amylase_C; 1.
Pfam; Pr02903; alpha-amylase_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M57692; AAB00841.1; -.
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SM00632; Aamy_C; 1.
SM00060; FN3; 2.
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Matches 133; Conserv
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                                                                                        NOPGSOSS FTAVT I EGMRVML FTHPLN FKGRWLRDRLNLWLTDNQR I YNVGQVS I GDENS
                                                                                                                       CTPADPAASSSERGCGPAVTTVGLVGFLSHSATKTEWEDAYRCVNASTANAERVPNGLKF
                                                                                                                                                                              576 GSVYIDGEPLEGSGQTVVPDGRTPDISHFYVG----GYGRSDMPTISHVTVNNVLLY-NR
                                                                         361 AYSSVLYKDD-----KLYCLHEINSNEVYSLVFARLVGELRIIKSVLQSWKNWDSHLSSI
                                                                                                                                                                 AGVGGGALWPVSQQGQNQRYHPANHAFTLVASVTIHEVPSVASPLLGASLDS-----
                                                                                                                                                                                                             --SGGKKLLGLSY------DEKHQWQ--PIYGSTPVTPTGSWEMGKRYHVVLTMANKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Igdoura S.A., Gafuik C., Mertineit C., Saberi F., Pshezhetsky A.V., Potter M., Trasler J.M., Gravel R.A.; "Cloning of the cDNA and gene encoding mouse lysosomal sialidase and correction of sialidase deficiency in human sialidosis and mouse SM/J
                                                      ---STDNVGIYDY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98029867; PubMed=9363440; Carrillo M.B., Milner C.M., Ball S.T., Snoek M., Campbell R.D.; "Cloning and characterization of a sialidase from the murine histocompatibility-2 complex: low levels of mRNA and a single amino acid mutation are responsible for reduced sialidase activity in mice
                                                                                                                                                                                                                                                                                                                                                                                       035657; 055220; Q99KG9; 28-FBB-2003 (Rel. 41, Created) 28-FBB-2003 (Rel. 41, Last sequence update) 110-0CT-2003 (Rel. 42, Last annotation update) Sialidase 1 precursor (EC 3.2.1.18) (Lysosomal sialidase) (N-acetyl-alph-neuraminidase 1) (G9 sialidase).
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Schaffer T., Ratciliffe A., Abbasi N., Loretz C., Lasky S., Hood L.;
"Sequence of the mouse MHC class III region."
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI TaxID=10090;
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                                                      NOPGTESS -----RVSLTWNP-
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MEDLINE=98046014; PubMed=9384611;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carrying the Neula allele."; Glycobiology 7:975-986(1997).
                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altachul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Shat N.K.,
Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Altschul S.P., Zeeberg B., Bonaldo M.F., Carning L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carning L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carning L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carning L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKenan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Butfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length
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DOWAIN: A C-terminal internalization signal (YGTL) appears to allow the targeting of plasma membrane proteins to endosomes. FTM: N-glycosylated (Probable).

FTM: Phosphorylation of tyrosine within the internalization signal
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CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosaid linkages of terminal stallc residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
SUBDWIT: Interacts with cathepsin A (protective protein), beta-
galactosidase and N-acetylgalactosamine-6-sulfate sulfatase in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        results in inhibition of sialidase internalization and blockage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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EMBL; BC004666; AAH04666.1;
HSSP; Q02834; 1EUR.
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InterPro; IPR002860; GF
Pfam; PF02012; BNR; 4.
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51 VHSFRLPALVNVD-GVMVAIADARYETSNDNSLIDTVAKYSVDDGETWETQIAIKNSRAS 109
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MEDLINE=97001677; PubMed=8844669;
Smith L.E., Uemura H., Eichinger D.;
"Isolation and expression of an open reading frame encoding sialidase
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
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MEDLINE=93010978; PubMed=1396577;
UGMUTA H.; SChenkman S., Nussenzweig V., Bichinger D.;
UGMUTA H.; Schenkman S., Nussenzweig V., Eichinger D.;
"Ohly some members of a gene family in Trypanosoma cruzi enco
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Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
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Mol. Biochem. Parasitol. 79:21-34(1996).
EMBL; D50685; BAA03334.1; -.
EMBL; D50685, 228409.
PPB; S28409; S28409.
PDB; LMS0; 25-MAR-03.
GO; GO:0004308; F:exo-alpha-sialidase activity; IEA.
GO; GO:0009405; P:pathogenes1s; IEA.
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Q27064 trypanosoma
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sp human:*
sp invertebrate:*
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SLIDTVAKYSVDDGETWETQIAIKNSRASSVSRVVDPTVIVKGNKLYVLVGSYNSSRSYW 140
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"Isolation and expression of an open reading frame encoding sialidase from trypanosoma rangeli.";
Mol. Biochem. Parasitol. 79:21-34(1996).

EMBL; D50684; BAA09333.1;
EMBL; D50684; BAA09333.1;
EMBL; D50684; BAA09333.1;
EMBL; D50684; BAA0933.1;
Interpro; DFR008405; P:pathogenesis; IEA.
Interpro; IPR008405; Cond. like_lec_gl.
Interpro; IPR00856; Cond. like_lec_gl.
Interpro; IPR008056; Cond. like_lec_gl.
Interpro; IPR008037; Sialidase_trypan.
Pfam; PF02012; BRN; 3.
PRINTS; PR01803; TCSIALIDASE.
SEQUENCE 964 AA; 101611 MW; 8P0600289FB847AD CRC64;
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Best Local Similarity 97.5%; Pred. No. 2.9e-225;
Matches 631; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                          STRAIN=Y;
MEDLINE=97001677; PubMed=8844669;
               [2]
SEQUENCE OF 178-378 FROM N.A.
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
NCBI_TaxID=5693;
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35.5%; Score 3360; DB 5; Length 1060;
al Similarity 99.2%; Pred. No. 1.6e-229;
642; Conservative 2; Mismatches 3; Indels 0
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Last sequence update)
Last annotation update)
InterPro; IPR008985; ConA like_lec_gl.
InterPro; IPR002860; GH_BNR.
InterPro; IPR008377; Slalidase_trypan.
PFam; PF02012; BNR; 3.
PRINTS; PR01803; TCSIALIDASE.
SEQUENCE 1060 AA; 110103 MW; EBD14
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   542 MGKRYHVVLTMANKIGSEYIDGEPLEGSGQTVVPDERTPDISHFYVGGYKRSDMPTISHV 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cremona M.L., Sanchez D.O., Frasch A.C., Campetella O.; "A single tyrosine differentiates active and inactive Trypanosoma cruzi trans-sialidases.";
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EMBL; L38457; AAA99443.1; -.

EMBL; L38457; AAA99443.1; -.

GO; GO:0004405; F:exc-alpha-sialidase activity; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

InterPro; IPR008985; ConA like_lec_gl.

InterPro; IPR008985; ConA like_lec_gl.

InterPro; IPR008977; Sialidase_trypan.

PFam; PF02012; BNR; 3.

PRINTS; PR01803; TCSIALIDASE.

SEQUENCE 642 AA; 70459 MW; 09F047336492081B CRC64;
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                                                                                                                    641
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                                                                                        TVNNVLLYNRQLNAEEIRTLFLSQDLIGTEAHMDSSSDTS
                                                          TVNNVLLYNROLNAERIRTLFLSQDLIGTEAHMGSSSGSS
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Pred. No. 2.9e-223;
6; Mismatches 9;
                                                                                                                                                                                                                                                                 642 AA
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MEDLINE=95354943; PubMed=7628705;
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ilarity 97.7%;
Conservative
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Best Local Similarity
Matches 625; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 VAIVASNGNLVYPVQVTNYKKQVFSKIFYSEDEGKTWKFGKGRSAFGCSEPVALEWEGK
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                                                                                                                                                                                                                                                                                                                     Trypanosoma cruzi.
Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
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A Campetella O.E., Uttaro A.D., Paradi A.J., Frasch A.C.;

A campetella O.E., Uttaro A.D., Paradi A.J., Frasch A.C.;

A recombinant Trypanosoma cruzi trans-sialidase lacking the acid repeats retains the enzymatic activity.";

L Mol. Blochem. Parasitol. 64:337-340(1994).

R PDB; IMRS; 18-MAR-03.

R PDB; IMRS; 18-MAR-03.

R GO; GO:0009405; P:pathogenesis; IEA.

R InterPro; IPR002860; GH BNR.

R InterPro; IPR008377; Siālidase_trypan.
TVNNVLLYNRQLNAEEIRTLFLSQDLIGTEAHMDSSSDSNAHSTPST 679
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NCBI_TaxID=5693;
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X MEDLINE-9534943; PubMed=7628705;

X Cremona M.L., Sanchez D.O., Frasch A.C., Campetella O.;

T. A single tyrosine differentiates active and inactive Trypanosoma oruzi trans sialidases.";

T Cruzi trans sialidases.";

Gene 160:123-128(1985).

R MBL; L38456; AAA942.1;

R RGJ; GO:0004108; F:exo-alpha-sialidase activity; IEA.

R GO; GO:0004108; F:exo-alpha-sialidase activity; IEA.

R GO; GO:000405; P:pathogenesis; IEA.

InterPro; IRR002865; ConA like_lec_gl.

R InterPro; IRR008985; ConA like_lec_gl.

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P Fam; PRO2012; BNR; 3.

R RINTS; PRO1803; TCSIALIDASE.
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NCBI_TaxID=5693;
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SEQUENCE FROM N.A.

STRAIN=Tulahuen;

CRAIN=Jahuen;

MEDLINE=5354943; PubMed=7628705;

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Tremona M.L., Sanchez D.O., Frasch A.C., Campetella O.;

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Tremona M.L., Sanchez D.O., Frasch M.L.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 MAPGSSRVELFKROSSKVPFEKGGKVTERVVHSFRLPALVNVDGVMVALADARYETSNDN
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
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93.4%; Pred. No. 1e-213;
ive 21; Mismatches 20; Indels
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0004108; F:exo-alpha-sialidase activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008965; ConA like_lec_gl.
InterPro; IPR008965; ConA like_lec_gl.
InterPro; IPR0089377; Sialidase_trypan.
Pfam; PP02012; BNR; 3.
PRINTS; PR01803; TCSIALIDASE.
SEQUENCE 643 AA; 70546 MW; E46D9A7CE9218ECB CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                      643
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Matches 599; Conservative 2
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TCTS.
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01-JUN-2001
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01-OCT-2003
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                                                                       GFLSHSATKTEWEDAYRCVNASTANAERVPNGLKFAGVGGGALWPVSQQGQNQRYHFANH
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
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Kim D.H., Santos M.R.M., Araya J.E., Souza R.T., Gomes H.B.M.,
Good N., Kelly J.M., Franco da Silveira J.;
Submitted (JUN-2002) to the EMEL/GenBank/DDBJ databases.
EMEL; AF525766; AAP80764.1; -.
Hypothetical protein.
EXQUENCE 892 AA; 94623 MW; F9B45DA3EDDF1181 CRC64;
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Last sequence update)
Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein.
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es 611; Conservative 1
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RP SEQUENCE FROM N.A.

RX MEDLINE=97001677; PubMed=8844669;

RA Smith L.E., Uemura H., Eichinger D.;

RI "Isolation and expression of an open reading frame encoding sialidase from Trypanosoma rangell.";

Mol. Biochem. Parasitol. 79:21-34(1996).

BR MBL, D56686; BAA0335.1; -.

DR GO; GO:00004108; F:exo-alpha-sialidase activity; IEA.

BR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR002860; GH BNR.

DR InterPro; IPR002877; Sialidase_trypan.

BR Ffam; PF02012; BNR; 2.
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NCBI_TaxID=5693;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Trans-sialidase homolog (Fragment).
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83.0%; Score 2920; DB 5;
Best Local Similarity 86.7%; Pred. No. 1.4e-198;
Matches 556; Conservative 27; Mismatches 58;
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NCSI_TaxID=5693;
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Mol. Biochem. Parasitol. 47:247-250(1991).
EMBL, X37235; SZA40511.1;
PIR, S33006, SZA3006.
R GO; GO:0004308; F:exc-alpha-sialidase activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR002860; GH BNR.
InterPro; IPR002860; GH BNR.
InterPro; IPR002860; GH BNR.
R InterPro; IPR00383; TCSIALIDASE.
R PRINTS; PR01803; TCSIALIDASE.
SEQUENCE 879 AA; 93939 MW; SE7255CA4C94D66E CRC64;
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Last annotation update)
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MEDLINE=92049558; PubMed=1840626;
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SEQUENCE FROM N.A.
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Best Local Similarity 84.6
Matches 543; Conservative
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 TSHGDARDWDI1LLAVGEVTKSTAGGKITASIKWGSPVSLKEFFPAEMEGMHTNQFLGGAG
                     TWQPDGSDWRPMLAVGEVTKSTADGKTTANITWGSPVSLKEFFPAEMEGMHTKQFLGGAG
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Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
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Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases.
EMBL, U01098; AAC98544.1; -
GO; GO:0004908; F:exc-alpha-sialidase activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
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Mol. Biochem. Parasitol. 70:9-17(1995)
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MEDLINE=95364855; PubMed=7637718;
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MEDLINE=95395867; PubMed=7666441;
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SEQUENCE OF 124-324 FROM N.A.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Sialidase precursor (EC 3.2.1.18) (EXO-alpha-sialidase)
(Neuraminidase) (N-acylneuraminate glycohydrolase) (Alpha-
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84.6%; Pred. No. 2.8e-193;
ive 29; Mismatches 70;
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MEDLINE=98115452; PubMed=9455917;
Buschiazzo A., Campetella O., Frasch A.C.C.;
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InterPro; IPR002860; GH BNR.
InterPro; IPR008377; Sialidase_trypan.
Pfam; PP02012; BNR; 2.
Pfam; PR01803; TCSIALIDASE.
SEQUENCE 736 AA; 81997 MW; 75A8026
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ERBL, U83180; AACS5493.1; -.

BRE, U83181; AACS5493.1; -.

BRE, U83181; AACS5493.1; -.

BRE, U83181; AACS5493.1; -.

BRE, URS5; 16-OCT-02.

BRE, URS5;
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23 660 SIALIDASE.
660 AA; 71964 MW; BSD55765DC4423D0 CRC64;
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  cloning,
    "Trypanosoma rangeli sialidase:
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SIGNAL
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Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5698;
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STRAIN-Venezuelan El Tocuyo;
STRAIN-Venezuelan El Tocuyo;
STRAIN-Venezuelan El Tocuyo;
MEDLINE=97001677; PubMed-8844669;
A MIDLINE=97001677; PubMed-8844669;
A Midline and expression of an open reading frame encon from Trypanosoma rangeli.";
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                                 Created)
Last sequence update)
Last annotation update)
SHVTVNNVLLYNRQLNAEEIRTLFLSQDLIGTEAHMGSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.2%; Score 2259; DB 5;
69.9%; Pred. No. 9.8e-152;
iive 68; Mismatches 114;
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PRINTS; PR01803; TCSIALIDASE.
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
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         ANHAFTLVASVTIHEVPSVASPLLGASLDSSGGKKLLGLSYDEKHQWQPIYGSTPVTPTG
                                                                 SWEMCKRYHVVLTMANKIGSVYIDGEPLEGSGQT---VVPDGRTPDISHFYVGGYGRSDM
                                                                                                          SWKIHQTYHVALLFPQGVGSIYIDGNLLKGSGQILSGVHLEGL--DVSHPFFGRYGTSDL
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAINS-Venezuelan B1 Tocuyo;
MEDLINE-97001677; PubMed=8844669;
Smith L.E., Uemura H., Eichinger D.;
"Isolation and expression of an open reading frame encoding sialidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHMAPGSSRVELFKRQSSKVPPEK-GGKVTERVVHSPRLPALVNVDGVMVAIADARXETS
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                                                                                                                                                                                                                                                                                             Trypanosoma rangeli.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5698;
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                                                                                                                                            661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 52.7%; Score 1853; DB 5; Length 6 Best Local Similarity 61.3%; Pred. No. 7.2e-123; Matches 374; Conservative 60; Mismatches 132; Indels
                                                                                                                                                         SOCHITYTNVMLYNRILKPNRIOTLLLS-----LGKTAADSE
                                                                                                                                            615 PTISHVTVNNVLLYNRQLNAEBIRTLFLSQDLIGTEAHMGSSSGSSE
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SEQUENCE 649 AA; 70872 MW; 26987D3786220004 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0004308; F:exo-alpha-sialidase activity; IEA. GO; GO:0009405; P:pathogenesis; IEA. InterPro; IPRO02860; GH BNR. FREEPER: IPRO088377; Sialidase_trypan. PF02012; BNR; 3.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                           649
                                                                                                                                                                                                                                                                                                                                                                                              from Trypanosoma rangeli.";
Mol. Biochem. Parasitol. 79:21-33(1996)
EMBL; U46073; AAC47214.1; -.
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
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          EMGKRYHVVLTMANKIGSVYIDGEPLEGSGQTVVPDGRTPDISHPYVGGYGRSDMPTISH
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                                                                                                                                                                                                                                               Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.4%; Score 2160.5; DB 5; Length 700; 64.5%; Pred. No. 1.2e-144; ive 68; Mismatches 147; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       700 AA; 77356 MW; BA34581AE138E97C CRC64;
                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
LDG trans-sialidase homologue.
                                                                                                                                                                    700 AA
                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=LDG;
MEDLINE=94158961; PubMed=8114811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 68.58;
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                                                                                     VTVNNVLLYNRQ 631
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PRINTS; PR01803; TCSIAI
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Search completed: August 3, 2004, 09:39:53 Job time: 44 secs

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161
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August 3, 2004, 09:36:35; Search time 21 Seconds (without alignments) 3064.387 Million cell updates/sec
                                                                                                                                       1 MGSSHHHHHHHSSGLVPRGSH.....EAHMGSSSGSSERSTPGSGC
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Compugen Ltd.
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Copyright (c) 1993 - 2004
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Gapop 10.0 , Gapext 0.5
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3517
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Minimum DB seq length: 0 Maximum DB seq length: 200000000

trypomastigote-spe trypomastigote sur FL-160-2 protein -flagellum-associat surface protein -surface antigen gp FL-160-4 protein -85K surface antige exo-alpha-sialidas exo-alpha-sialidas
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exo-alpha-sialidas shed acute-phase a exo-alpha-sialidas transsialidase-neu Description SUMMARIES \$23006 JH0557 A45596 A45596 S44237 33082 S31082 S321082 S32148 S01339 S0 B * Query Match Length D Score No.

exo-alpha-Bialidas probable secreted neuraminidase B [i FL-160 protein - T FL-160 protein - T	Avicelase III - As sialidase - Actino FL-160 protein - T exo-alpha-sialidas exo-alpha-sialidas neuraminidase vin euraminidase vC17 flagellum-associat FL-160-1 protein - flagellum-associat neuraminidase, pro	ALIGNMENTS RESULT 1 S23006 shed acute-phase antigen - Trypanosoma cruzi c;becies Trypanosoma cruzi C;becies Trypanosoma cruzi C;becies Trypanosoma cruzi C;bate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999 C;Accession: 523006 R;Pollevick, G.D.; Affranchino, J.L.; Frasch, A.C.C.; Sanchez, D.O. A;Title: The complete sequence of a shed acute-phase antigen of Trypanosoma cruz A;Reference number: S23006; MUID:92049558; PMID:1840626 A;Accession: S23006 A;Cosserefamily: trypomastigote-specific surface antigen
B98063 T37097 E95196 S36036	T00349 749227 S36033 JE0387 S20590 A43866 E2158 S32015 PH1917 A41111	ALIGNMENTS RESULT 1 S23006 shed acute-phase antigen - Trypanosoma cruzi C;Species: Trypanosoma cruzi C;Date: 17-Apr-1993 #sequence_revision 17-Apr- C;Accession: S23006 R;Pollevick, G.D.; Affranchino, J.L.; Frasch, R;Pollevick, G.D.; Affranchino, J.L.; Frasch, A;Ttle: The complete sequence of a shed acute A;Reference number: S23006; MUID:92049558; PMI A;Accession: S23006 A;Accession: S23006 A;Accession: S23006 A;Accession: S23006 A;Accession: S23006 C;Superfamily: trypomastigote-specific surface
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161 159 157 153.5	151.5 145.5 143.5 143.5 140.5 134 129 129	RESULT 1 \$23006 shed acute-phase antigen - T C;Species: Trypanosoma cruzi C;Accession: \$23006 R;Pollevick, G.D.; Affranchi Mol. Biochem. Parasitol. 47, A;Title: The complete sequen A;Reference number: \$23006; A;Accession: \$23006 A;Molecule type: DNA
9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	RESULT 1 S23006 shed acute-pb C;Species: Tz C;Date: 17-Ag C;Accession: R;Pollevick, Mol. Biochem A;Title: The A;Accession: A;Accession: A;Accession: A;Accession: A;Kresidues: 1 A;Cross-refex C;Superfamily

21.

Length 879;

Score 3093.5; DB 2; Pred. No. 2.5e-215;

88.0%; 91.5%;

Query Match Best Local Similarity

N	re 21; Mismatches 33; Indels 1; Gaps 1;	MAPGSSRVELFKRQSSKVPFEKGGKVTBRVVHSFRLPALVNVDGVMVAIADARYETSNDN 80	:	ARYSVDDGETWETQIAIKNSRASSVSRVVDPTVIVKGNKLYVLVGSYNSSRSYW 140	SLIDTVVKYSVDOGETWETQIAIKNSRASSVSRVVDPTVIVKGNKIYVLVGSYNSSTSYW 152	TSHGDARDMDILLAVGEVTKSTAGGKITASIKWGSPVSLKEFFPAEMEGMHTNQFLGGAG 200	TSHGDARDWDILLAVGEVTKSIVDGKTTANITWGSPVSLKEFFPAYMEGWHTNQFLGGAG 212	COVESKIFYSEDEGKTWKFG	VAIVASNGNLVYPVQVTNKRKQVFSKIFYSEDDGKTWKFGKGRSDFGCSEPVALEWEGKL 272	IINTRVDYRRRLVYESSDMGNSWVEAVGTLSRVWGPSPKSNQPGSQSSFTAVTIEGMRVM 320		LFTHPLNPKGRWLRDRLNLWLTDNQRIYNVGQVSIGDENSAYSSVLYKDDKLYCLHEINS 380	LFTHPLNFKGWALRDRLNLWITDNQRIYNVGQLSIGDENSAYSSVLYKDDKLYCHBINS 392	NEVYSLVFARLVGELRIIKSVLQSWROWDSHLSSICTPADPAASSERGCGPAVTTVGLV 440	NEVYSLVFARLVGELRIIKSVLQSWKKWDSHLSSICTPADPAASSSERVCGPAVTYGLA 452	GFLSHSATKTEWEDAYRCVNASTANAERVPNGLKFAGVGGGALWPVSQQGQNQRYHFANH 500	
	592; Conservative 21;	21 MAPGSSRVELFKROSSKVPFEK	:	81 SLIDTVAKYSVDDGETWETQIA	93 SLIDTVVKYSVDDGETWETQIA	141 TSHGDARDWDILLAVGEVTKST	153 TSHGDARDWDILLAVGEVTKSI	201 VAIVASNGNLVYPVQVTNKKK	213 VAIVASNGNLVYPVQVTNKRKÇ	261 IINTRVDYRRRLVYESSDMGNS	273 IINTRVDYRRRLVYESSDTEKP	321 LFTHPLNFKGRWLRDRLNLWLT	333 LFTHPLNFKGWWLRDRLNLWLT	381 NEVYSLVPARLVGELRIIKSVL		441 GFLSHSATKTEWEDAYRCVNAS	

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CiSpecies: Trypanosoma cruzi
CiSpecies: Trypanosoma cruzi
CiDate: 22-Apr-1993 #sequence_revision 02-Jun-1994 #text_change 16-Jul-1999
CiAccession: A5256; S27857
SiFouts, D.L.; Ruef, B.J.; Ridley, P.T.; Wrightsman, R.A.; Peterson, D.S.; Manning, J.B
Mol. Biochem. Parasitol. 46, 189-200, 1991
A;Title: Nucleotide sequence and transcription of a trypomastigote surface antigen gene
A;Reference number: A45596; MUID:92018016; PMID:1717846
A;Molecule type: DNA
                                                                                                                                                                                                                                                                    C;Species: Trypanosoma cruzi
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-Jan-2000
C;Dates 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-Jan-2000
R;Genura, H.; Schenkman, S.; Nussenzweig, V.; Eichinger, D.
EMBO J. 11, 3837-3844, 1992
A;Title: Only some members of a gene family in Trypanosoma cruzi encode proteins that A;Reference number: S28409; MUID:93010978; PMID:1396577
                               61 IFYSEDEGKTWKFGEGRSDFGCSEFVALEWEGKLINTRVDYRRRLVYESSDMGNSWVEA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Gene: TSA-1
C;Superfamily: trypomastigote-specific surface antigen
C;Keywords: surface antigen
P;1-28/Domain: signal sequence #status predicted <SIG>
F;29-835/Froduct: trypomastigote-specific surface antigen #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 ITASIKWGSPVSLKEFFPAEMEGMHTNQFLGGAGVAIVASNGNLVYPVQVTNKKKQVFSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 IFYSEDEGKTWKFGEGRSDFGCSEPVALEWEGKLIINTRVDYRRRLVYESSDMGNSWVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGTLSRVWGPSPKSNQPGSQSSFTAVTIEGMRVMLFTHPLNFKGRWLRDRLNLWLTDNQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-835 crOU>
A;Cross-references: EMBL:M58466; NID:g162314; PIDN:AAA30259.1; PID:g162315
A;Experimental source: strain Peru
A;Note: sequence extracted from NCBI backbone (NCBIN:61039, NCBIP:61041)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   trypomastigote-specific surface antigen precursor - Trypanosoma cruzi
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26.1%; Score 918; DB 1; Length 835;
Best Local Similarity 35.6%; Pred. No. 4.4e-58;
Matches 250; Conservative 107; Mismatches 256; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-200 CUEM>
C;Superfamily: trypomastigote-specific surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1057; DB 2;
Pred. No. 4.3e-69;
                                                                                                                                                                                                                                                 transsialidase-neuraminidase - Trypanosoma cruzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
30.1%; Score 1057; D
Best Local Similarity 100.0%; Pred. No. 4.3
Matches 200; Conservative 0; Mismatches
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                                                                                                              661 ERSTPGS 667
                                                                                                                                                     596 AHSTPST 602
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C.5Species: Trypanosoma cruzi
C.5Species: Trypanosoma cruzi
C.5Species: Trypanosoma cruzi
C.5Accession: JH0557
M.E.A.; Mejla, J.S.; Ortega-Barria, E.; Matzilevich, D.; Prioli, R.P.
J. Exp. Med. 174, 179-191, 1991
A.Title: The Trypanosoma cruzi neuraminidase contains sequences similar to bacterial neu
A,Reference number: JH0557
MACCESSION: JH0557
A,Molecule trype: DNA
A,Residues: 1-116.2 BERA
A,Residues: 1-116.2 BERA
A,Residues: 1-116.2 BERA
A,Residues: GB:WG1732; NID:9162302; FID:9162303
A,Robe: the authors translated the codon TCT for residue 45 as Cys
C,Comment: This protein plays a role in parasite-host cell interaction.
C,Superfamily: trypomastigote-specific surface antigen
C,Superfamily: trypomastigote-specific surface antigen
C,Superfamily: alycoprotein; Glycosidase; hydrolase
F;394/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ned
                                             572
                                                                        561 MGKRYHVVLTMANKIGSVYIDGEPLEGSGQTVVPDGRTPDISHFYVGGYGRSDMPTISHV 620
                                                                                                 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYVLVGSYNSSRSYWTSHGDARDWDILLAVGEVTKSTAGGKITASIKWGSPVSLKEFFPA 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 OSSFTAVTIEGMRVMLFTHPLNFKGRWLRDRLNLWLTDNORIYNVGQVSIGDENSAYSSV 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMEGMHTNOFLGGAGVALVASNGNLVYPVQVTNXKKQVFSKIFYSEDEGKTWKFGEGRSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 LYKDDKLYCLHEINSNEVYSLVPARLVGELRIIKSVLQSWKNWDSHLSSICTPADPAASS
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                                                                                                                                                   76.2%; Score 2681; DB 2; Length 1162;
86.5%; Pred. No. 2.6e-185;
rative 22; Mismatches 50; Indels 10
  AFTLVASVTIHEVPSVASPLLGASLDSSGGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 86.5*
Matches 525; Conservative
501
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A,Accession: JH0823
A,Molecule type: DNA
A,Residues: 1-1003 «VAN»
A,Cross-references: GB:X70948; NID:g11159; PID:g531496
A,Note: in the authors' translation, the protein sequence has an additional Val between
C;Keywords: glycoprotein
F;49,81,85,105,198,255,475,490,584,937,952/Binding site: carbohydrate (Asn) (covalent)
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                                                                                                                                                                                                                                                                                                                                                                                  274 SVGCRSPRITEWEEDILMVIYCEDGRK-VFESRDWGKTWIKAVRILSGVWLKSGPELPEV 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : || |||| ::| || ||| 333 SLRVDALITA-TIEGRKVMLYTQKVR---HFLEVDEPNALHLWVTDNNRTFHLGPFSVDS 388
                                                                                                                                                   LVGSYNSSRSYWTSHGD----ARDWDILLAVGEVTKSTAGGKITASIKWGSPVSLKEFFP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 QPGSQSSFTAVTIEGMRVMLFTHPLNFKGRWLR----DRLNLWLTDNQRIYNVGQVSIGD 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -ENSAYSSVL-YKDDKLYCLHEINSNEVYSLVFARLVGELRIIKSVLQSWKNWDSHLSSI 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         416 CTPADPAASSSERGCGPAVTTVGLVGFLSHSATKTE-WEDAYRCVNASTANAERVPNGLK 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLSYDEKHQWQPIYGSTPVTPTGSWEMGKRYHVVLTM--ANKIGSVYIDGEPLEGSGQTV 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 IAMFVPKKTQVVPKSGGE--GKVKDIFASPALVRAGGVMIAFVEGRTKHTDFPEAIDLSS 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FL-160-2 protein - Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 29-Jan-1999
C;Accession: JM0823
R;Van Voorhis, W.C.; Barrett, L.; Koelling, R.; Farr, A.G.
J. Exp. Med. 178, 681-694, 1993
A;Fitle: FL-160 proteins of Trypanosoma cruzi are expressed from a multigene
A;Reference number: JH0823; MUID:93340646; PMID:7688032
                                                  IDTVAKYSVDDGETWETQIA------IKNSRASSVSRVVDPTVIVKGNKLYV
                                                                                                                                                                                                                                                                                    215 PNNKG-DLKEFLGGGGGGIVMGNGTLVFPRTAKDENNKVVSLITYSTDDGQKWEIPGGVS
                                                                                                                                                                                                                                                                                                                                                       245 DFGCSEPVALEWEGKLIINTRVDYRRRLVYESSDMGNSWVEAVGTLSRVW---GPSPKSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                552 GLSYGAGGKWETVYDGTKTVQGGTWEPGREYQVALMLQDGNK-GFVYVDGVLVGNPAMLP
                                                                                                                                                                                                                                                      185 AEMEGMHTNOFLGGAGVAIVASNGNLVYPVQVTNKKKQVFSKIFYSEDEGKTWKFGEGRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            665 SGDSEDKKESGDSE 678
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Best Local S
Matches 237
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CiSpecies: Trypanosoma cruzi
CiSpecies: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
CiAccession: 544237
R.Nickell, S.P.; Keane, M.A.
R.Nickell, S.P.; Keane, M.A.
R.Nickell, S.P.; Keane, M.A.
R.Nickell, S.P.; Keane, M.A.
R.Nickell, S.P.; Keane, M.A.
R.Nickell, S.P.; Keane, M.A.
R.Nickell, S.P.; Keane, M.A.
R.Nickell, S.P.; Keane, M.A.
R.Nickell, S.P.; Keane, M.A.
R.Nickell, S.P.; Keane, M.A.
R.Nickell, S.P.; Keane, M.A.
R.Nickell, S.P.; Keane, M.A.
R.R.Nickell, S.P.; Keane, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HVVLTM--ANKIGSVYIDGEPLEGSGQTVVPDGRTPDISHFYVGGYGRSDMPTISHVTVN 623
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                                                                                                                                                                                                                                                            VNVDGVMVAIADARYETSN-----DNSLIDTVAKYSVDDGETWETQIA-----
                                                                                                                                                                                                                              --IKNSRASS----VSRVVDPTVIVKGNKLYVLVGSYNSSRSYWTSHGDARDWDILLLAVG
                                                                                                                                                                                                                                                                                                                                    EVTKSTAGGKITASIKWGSPVSLKEFFPAEMEGMHTNQFLGGAGVAIVASNGNLVYPVQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       447 ATKTE-WEDAYRCVNASTANAERVPNGLKFAGVGGGALWPVSQQGQNQRYHFANHAFTLV
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                        GSSHHHHHHSSGL-VPRGSHMAPGSSRVELFKRQSSKVPFEKG-GKVTERVVHSFRLPAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       624 NVLLYNRQLNAEEIRTLFLSQDLIGTEAHMGSS-----SGSSE 661
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Matches 237; Conserv
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ò 8	168 TASIKWGSPVSLKEFFPAEMEGMHTNQFLGCAGVAI-VASNGNLVYPVQVTNKKK 221	ò a	
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g ò	355 LWLSDMORIYDVGQISAENEDVAASTLLYATVEVPSLEGGERKGERKÄLYČSYEVAAAEDG 414 383 VYSLVFARLVGELRIIKSVLQSWRAWDSHLSSICTPADPAASSSERGCGPAVTTV 437	a 8	TSCDDGBRAYESTMGNLMYEEYDTLSRVWGNSLKRTGHGVQGGFVSATINGQKVILVS
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è a	438 GLVGFLSHSATKTEWEDAYRCYNAST-ANAERVPN-GLKFAGVGGGALWPVSQQGQNQRY 495 :	& 8	368 -KDDKLYCLHEINSNEVYSLVFARLVGELRIIKSVLQSWKNWDSHLSSICTPADPAAS 424 :: : : : : : :
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qa	707 EVPAPEGAPEKS 718	q	
RESULT 7 S32016 flagellum C;Species	-associated protein - Trypanosoma cruzi (fragment)	ço qa	633 NAEEIRTLFLEQDLIGTEAHMGSSGSSERS 663 : :
C;Date: 0 C;Accessi R;van Voo submitted A:Descripi	ge 01-Dec-2000	RESULT 8 T30521 surface C;Specie	protein - Trypanosoma cruzi 8: Trypanosoma cruzi
A; Referen A; Accessic A; Status:	ssed from a multigene famil	C,Date: C,Access R,Gao, G	22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000 lon: T30521 ; Nara, T.; Nakajima-Shimada, J.; Aoki, T.
A; Molecul A; Residue A; Cross-re		J. Mol. A,Title: A,Refere	of five;
R; Van Voo. J. Exp. M. A; Title: 1 A; Reference	R; Van Voorhis, W.C.; Barrett, L.; Koelling, R.; Farr, A.G. J. Exp. Med. 178, 681-684, 11993 A; Title: FL-160 proteins of Trypanosoma cruzi are expressed from a multigene family and A; Reference number: JH0823; MUID:93340646; PMID:7688032	A; Access A; Status A; Molecu A; Residu	JBJ
A; Residues C: Keywords		C;Superfamily Query Match	face antigen
Query Match	3: giftoprotein atch 25.1%; Score 881.5; DB 2; Length 959;		al 8 231
Matches	9; Conservat	상 음	34 QSSKVPFEKGGKVTERVVHSFRLPALVNVDGVMVAIADARYETSNDNSLIDTVAK 88

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FL-160-4 protein - Trypanosoma cruzi (fragment)
C;Species: Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Accession: PH1919; 832017
R;Van Voorhis, W.C.; Barrett, L.; Koelling, R.; Farr, A.G.
J;Exp. Med. 178, 681-694, 1993
A;Title: FL-160 proteins of Trypanosoma cruzi are expressed from a multigene family and A;Reference number: J0823; MUID:93340646; PMID:7688032
A;Accession: PH1919
A;Molecule type: DNA
A;Residues: 1-641 <VAN
R;Van Voorhis, W.C.; Barrett, L.; Koelling, R.; Farr, A.G.
Submitted to the EMBL Data Library, February 1993
A;Residues: 12-160 proteins of Trypanosoma cruzi are expressed from a multigene family A;Reference number: S32015
A;Accession: S32017
A;Residues: 1-280; LL., 291-309; NY, 311-641 <VA2>
A;Residues: 1-280; LL., 291-309; NY, 311-641 <VA2>
A;Residues: 1-280; LL., 291-309; NY, 311-641 <VA3>
A;Cross-references: EMBL:X70950; NID:911162; PID:911163
C;Keywords: 91ycoprotein
F;115,130,224,575,590/Binding site: carbohydrate (Asn) (covalent) #status predicted
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surface antigen gp85 - Trypanosoma cruzi
Cistace antigen gp85 - Trypanosoma cruzi
Cistace antigen gp85 - Trypanosoma cruzi
Cistace 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
C; Accession: A45622
R; Takle, G. B.; Cross, G.A.
R; Takle, G. B.; Cross, G.A.
Mol. Biochem. Parasitcl. 48, 185-198, 1991
A; Title: An 85-kilodalton surface antigen gene family of Trypanosoma cruzi encod
A; Reference number: A45622; MUD: 92107221; PMID: 1762630
A; Accession: A45622
A; Status: preliminary
A; Molecule type: mRNA
A; Residuence extracted from NCBI backbone (NCBIN: 74863, NCBIP: 74864)
C; Superfamily: trypomastigote-specific surface antigen
C; Keywords: surface antigen
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Db 346 NAEKEELESALLYSDGKLHLLORRVSGEGSVISLSRLTEELKEIESVLSTWAQKDIFFSS 405 Qy 415 ICTPADPAASSERGCGPAVTTVGLVGFLS 444 Db 406 LSIPTAGLVAVLS 418 RESULT 12 A37334 exo-alpha-sialidase (EC 3.2.1.18) - Clostridium sordellii C;Species: Clostridium sordellii C;Species: Clostridium sordellii C;Species: A37234 exo-alpha-sialidase (EC 3.2.1.18) - Clostridium sordellii C;Species: A37234 exo-alpha-sialidase (EC 3.2.1.18) - Clostridium sordellii C;Species: A37234 exo-alpha-sialidase (EC 3.2.1.18) - Clostridium sordellii C;Species: A37234 A;Title: Cloning, Sequence_revision 30-Dec-1991 #text_change 17-Mar-2000 R;Rothe, B.; Roggentin, P.; Frank, R.; Bloecker, H.; Schauer, R. J. Gen. Microbiol. 135, 3087-3096, 1989 A;Title: Cloning, Sequencing and expression of a sialidase gene from Clostridium sordell A;Status: preliminary A;Accession: A37234 A;Status: Preliminary A;Molecule type: DNA A;Residues: 1-404 <rot> A;Status: Preliminary A;Residues: 1-404 <rot> A;Status: Preliminary A;Residues: 1-404 <rot> A;Status: Preliminary A;Residues: 1-404 <rot> A;Cross-references: GB:M31S84; NID:G144910; PIDN:AAA22280.1; PID:G144911 C;Superfamily: trypomastigote-specific surface antigen C;Keywords: glycosidase; hydrolase</rot></rot></rot></rot>	Query Match	RESULT 13 80139 80131 80131 80131 80131 80131 80131 80131 80321.18) - Clostridium perfringens 80.41 80.41 80.41 80.42 80.43 80
	S25236 85K surface antigen - Trypanosoma cruzi (fragment) C; Species: Trypanosoma cruzi C; Species: Trypanosoma cruzi C; Species: Trypanosoma cruzi C; Species: Trypanosoma cruzi C; Species: Trypanosoma cruzi C; Species: Trypanosoma cruzi C; Species: Trypanosoma cruzi C; Species: Trypanosoma cruzi C; Species: Trypanosoma cruzi C; Species: Trypanosoma cruzi C; Species: Sizia Mol. Biochem: Parasitcol. 37, 57-64, 1989 A; Takle, G.B.: Young, A.: Snarty, D.: Hudson, L.: Nicholls, S.C. A; Rates: Cloning and expression of a trypomastigote-specific 85-kilodalton surface antig A; Racession: S25236 A; Racession: Samilarity A;	QY 129 LVGSYNSSRSYWTSHQDARDWDILLAVGEVTKSTAGCKITASIKWGSPVS-LKEFFPA 185

Length 382;

Query Match

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exo-alpha-sialidase (EC 3.2.1.18) - Salmonella typhimurium
N.Alternate names: neuraminidase
C;Species: Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 31-Dec-1992 #sequence
C;Accession: $20976; $233020; $23380; A33133
R;Hoyer, L.L.; Hamilton, A.C.; Steenbergen, S.M.; Vimr, B.R.
A;Title: Cloning, sequencing and distribution of the Salmonella typhimurium LT2 sialida
A;Reference number: $20976; MUID:9229952; PMID:1602967
                                                                                                                                                                                                                                                                                                          68 TAAARSTDGGKTWNKKIAIXNDRVNSKLSRVMDPTCIVANIQGRETILVWVGKWNNNDKT 127
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C;Keywords: glycosidase; hydrolase
F;2-376/Product: exo-alpha-sialidase #status experimental <MAT>
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Job time : 23 secs
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 270-299,301-357 <WAR>
A;Gene: nanH
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Matches 111; Conservative
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                                                                                        FRLP--ALVNVDGVMVAIADARYETSNDNSLIDTVAKYSVDDGETWETQIAIKNSRA-SS 110
                                                                                                                                                                                111 VSRVVD-PTVIVKGNKLYVLVGSYNSSRSY-WTSHGDARDWDILLAVGEVTKSTAGGKIT 168
                                                                                                                                                                                                       ASIKWGSPVSL-KEFFPAEMECMHTNQFLGGAGVAIVASNGNLVYPVQVT---NKKKQVF 224
                                                                                                                                                                                                                                                                                               145 NGLTWSNKIDLTKDSSKVKNQPSNTIGWLGGVGSGIVMDDGTIVMPAQISLRENNENNY 204
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C;Species: Clostridium perfringens
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 19-May-2000
C;Accession: S32148
                                                                                                               SKI FYSEDEGKTWKFGEGRSDFGCSEPVALEWEGKLI INTRVDYR-RRLVYESSDMGNSW
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10.2%; Score 359; DB 2; Length 382;
Best Local Similarity 28.4%; Pred. No. 3.4e-18;
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11.0%; Score 388; DB 2; Length 38 llarity 30.4%; Pred. No. 2.7e-20; Conservative 72; Mismatches 138; Indels
                  Local Similarity
nes 109; Conserv
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INV 10-JAN-2003

3183 bp DNA linear INV 10-JAN-200 Trypanosoma cruzi TCTS-154 gene for trans-sialidase, complete cds. D50685 D50685.1 GI:840707

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT D50685

ALIGNMENTS

Trypanosoma cruzi Trypanosoma cruzi Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma; Schizotrypanum. 1 (bases 534 to 1134) Uemura+H., Schenkman,S., Nussenzweig,V. and Bichinger,D. Only some members of a gene family in Trypanosoma cruzi encode proteins that express both trans-sialidase and neuraminidase

REFERENCE AUTHORS TITLE

X57235 T.CTLI She AJ002174 Trypanosome 105068 Trypanosome 108109 Trypanosome 10818 Trypanosome 104607 Trypanosome 104607 Trypanosome 104607 Trypanosome 10443 Trypanosome 10274 Trypanosome 10274 Trypanosome 101274 Trypanosome 101274 Trypanosome AC13260 Trypanosome AC13260 Trypanosome AC13260 Trypanosome AC097056 Trypanoso AC096945 Trypanoso AC096945 Trypanoso AC096945 Trypanoso AC096945 Trypanoso AC096945 Trypanoso AY186574 Trypanoso AR310232 Trypanoso U77911 Trypanosoma L14824 Trypanosoma MS8466 Trypanosoma AX289508 Trypanoso Z32744 T.cruzi gen L38457 Trypanosoma L38454 Trypanosoma L38456 Trypanosoma AF525766 Trypanoso AJ276679 Trypanoso X57235 T.cruzi she Trypanoso Trypanoso Trypanoso Trypanoso D50684 Trypanosoma L26499 Trypanosoma AR261980 Sequence Trypanoso Trypanoso Trypanoso Тгурапово score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description AC096778 1 AC097057 1 AF091620 1 AC104502 1 AF128843 1 AY186573 1 AR261979 SUMMARIES TRU46074
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TRB0B TRBTRSIC TRBTRSIA AF525766 TCR276679 TCSAPA TCJ002174 TRBTCNAA D50686 TCU01098 TCO535487 AC113260 AY142111 AC104490 AC097056 AC096945 AC097058 AF092099 AF091620 AC104502 AF128843 AY186573 AF181287 AY186574 D50685 AR261979 AC096778 AC097057 TRBTSA1 AY298908 TC85SUPR ICU77951 8 % Query Match Length D 3183 2895 1929 1929 1929 1929 1932 1932 2874 2100 2749 2620 22277 1833 22203 3245 940 601 131541 2939 19801 42075 32554 32126 3300 21765 28208 119452 119452 2150 2897 2140 3727 21700 2485 2133 1491 558.7 229.22.8 229.22.8 229.22.8 229.22.8 229.22.8 229.22.8 229.23 85.0 82.9 80.7 61.5 14.5 13.8 13.3 11.9 1900.6 1886.6 1886.6 1881.8 1877 1873.8 1756.6 1753.8 1708.2 1666 1622.2 1235.2 1185.8 1179 1121.4 1032.2 847.4 585 339.6 335 313 307.8 302.8 302.8 292.4 282.2 276.6 268.2 242.6 242.6 240.4 237.8 237.8 Score 263.8 264.2 Result υ υ U υu

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Direct Submission
Direct Submission
Submitted (27-MAY-1995) Haruki Uemura, Nagasaki University,
Institute of Tropical Medicine; 1-12-4 Sakamoto, Nagasaki, Nagasaki
B52, Japan (E-mail:H-Uemura@cc.nagasaki-u.ac.jp,
Tel:81-958-49-7837, Fax:81-958-49-7805)
Location/Qualifiers
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                                     Smith, L.E., Uemura, H. and Eichinger, D.
Isolation and expression of an open reading frame encoding stalidase from Trypanosoma rangeli
MOI. Blochem. Parasitol. 79 (1), 21-33 (1996)
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         (11), 3837-3844 (1992)
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GGGCGCTTTGGCCGGTGGGCCAGCAGCGCAATCAACGGTATCACTTTGCAAACCACGCGCGCG	& 4a	ATGTGGACGGGGTGATGCCATCGCGACGCTCGCTACGAACATCATGACAACT
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1562 TGGGTGCGAGCCTGGACTCTTCTGGTGGCAAAAACTCCTGGGGCTCTCGTACGACGAGA 1621 	රු සි	302 TTGCCATCAAGAACAGTCGTGCATCGTCTGTTTCTCGTGTGGATCCCACAGTGATTG 361
1622 AGCACCAGTGGCAGCCAATATACGGATCAACGCCGGTGACGCCGACCGGATCGTGGGAGA 1681 	S S	362 TGAAGGGCAACAAGCTTTACGTCCTGGTTGGAAGCTACAACACTTCGAGGAGCTACTGGA 421
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1982 AAAGAAGTACGCCGGATC 2000 2018 CCCACAGTACGCCTCAAC 2036	λ _ο	722 AGGIAGGAGIGATTITIGGCIGCIGCIGAACCIGIGGCCCTIGAGIGGGAGGGAAGCICA 781
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	S G	902 ACCAGCCCGGCAGTCAGAGCAGCTTCACTGCCGTGACCAGGGAATGCGTGTTATGC 961
REFERENCE 1 (bases 1 to 3183). AUTHORS Pelletier,M., Barker,W.A., Hakes,D.J. and Zopf,D.A. TITLE Methods for producing sialyloligosaccharides in a dairy source JOHRNAL Patent: US 6323008-A 1 27-NOV-2001;	cy da	962 TCTTCACACCCGCTGAATTTTAAGGGAAGGTGGCTGCGCGACCGAC
FEATURES LOCATION/QUALITIETS 13183	ç d	1022 TGACGGAFTAACAGCGCATTTATAACGTTGGGCAAGTATCCATTGGTGATGAAAATTCCG 1081
ore 1926.2; DB 6; Length 3183;	ò a	1082 CCTACAGCTCCGTCCTGTACAAGGATGATAAGCTGTACTGTTTGCATGAGATCAACAGTA 1141
1931; Conservative 0; Mismatches 8; Indels 0; Gaps 0; 62 TGGCACCCGGATCGAGCTGAGCTGTTAAGCGGCAAAGCTCGAAGGTGCCATTTG 121<	oy O	1142 ACGAGGTGTACAGCCTTGTTTTGCGCGCCTGGTTGGCGAGCTACGGATCATTAAATCAG 1201

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FANNAFTLYNASTTREWEDAYRCVNASTANAERVPNGLGGGONGRYF
FANNAFTLYNASTANAENTSTANAGLASLOSSGGKKLLGLSYDEKHOWOPIYGSTRS
DMFTISHTVNNVLLYNNGLNABEIRTLFLSGDLGTAHMDSSSDSNAHSTPSTFGG
SSAHSTPSTPADNGAHSTPSTPADNGAHSTPSTPDRANGAHSTPPTPA
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Submitted (27-MAY-1995) Haruki Uemura, Nagasaki University,
Institute of Tropical Medicine; 1-12-4 Sakamoto, Nagasaki, Nagasaki
B52, Japan (E-mail:H-Uemura@cc.nagasaki-u.ac.jp,
Tel:81-958-49-7837, Fax.81-958-49-7805)
Location/Qualifiers
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                                                                                      Smith, L.E., Uemura, H. and Eichinger, D.
Isolation and expression of an open reading frame encoding sialidase from Trypanosoma rangeli
Mol. Biochem. Parasitol. 79 (1), 21-33 (1996)
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/gene="TCTS-121"
/function="inactive trans-sialidase"
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/c1one="121"
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/organism="Trypanosoma c1/mol_type="genomic DNA"
/strain="Y"
                   (11), 3837-3844 (1992)
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Trypanosoma cruzi TCTS-121 gene for trans-sialidase, complete cds.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 54 to 1134)
Uemura, H., Schenkman, S., Nussenzweig, V. and Eichinger, D.
Only some members of a gene family in Trypanosoma cruzi encode
proteins that express both trans-sialidase and neuraminidase
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Qy 1382 CAAGCACGGCAAATGCGGAGAGGGTTCCGAACGGTTTGAAGTTTGCGGGGGTTTGGCGGAG 1441 Db 1418 CAAGCACGGCAAATGCGGAGAGGGTTCCGAACGGTTTGAAGTTTGCGGGGGTTGGCGAGG 1477 Qy 1442 GGGCGTTTGGCCGGTGAGCCAGCAGAGATCAACCACTTTGCAAACCACG 1501 Db 1478 GGGCGTTTGGCCGGTGAGCAGCAGAGAATCAACGGTACACTTTGCAAACCACG 1501 CD 1478 GGCGCTTTGGCCGGTGAGCAGAGAGAGAGATCAACGACTTTGCAAACCACG 1501 Db 1502 GGTTCACGCTGGTGACGAGACGATTCACGAGGTTCCGAGGTCGTTTGC 1561 CD 1538 GGTTCACGCTGGTGACTGGTGAATTCACGAGGTTCCGAGGTCGTTTGC 1597 CD 1562 TGGTTCACGCTGGTGGATTCAGTGAGTTCCGAGGTTCGTACGAGATCCTTTGC 1597 CD 1558 GGTTCACGCTGGTGGTGATTCAGTGAGTTCCTGGGGGTTTTTGCTTTTGC 1597 CD 1558 GGTTCACGGTGGTGGTTGGTGAATAAAACTCCTGGGGGTTTTTTTT	1622 AGCACCAGTGGCAGCCAATATACGGATCAACGCCGGTGACGCCGACCGGACCGGATCGTGGGAGAGA	1802 TCTCCCACTTCTAGGGGGGTATGGAAGAGTATGCCAACCATAAGCCAGGGA 1861	RESULT 4 TRBTKSI LOCUS DEFINITION TYPANOSOMA CTUZİ trANS-SIALİDASE GENE, COMPLETE CDB. DEFINITION TYPANOSOMA CTUZİ trANS-SIALİDASE GENE, COMPLETE CDB. LE6499 LE6499 LE6499 LE6499 LE6499 LE6499 LYPANOSOMA CTUZİ SOURCE TYPANOSOMA CTUZİ ORGANISM TYPANOSOMA CTUZİ ELKATYOCA; ENGLEOPLAYPANUM. TYPANOSOMA; CANDICALYPANUM. TYPANOSOMA; CANDICALYPANUM. TYPANOSOMA; CANDICALYPANUM. TYPANOSOMA; CANDICALYPANUM. TYPANOSOMA; CANDICALYPANUM. TYPANOSOMA; CANDICALYPANUM. TYPANOSOMA; CANDICALYPANOSOMA; JOURNAL MOI. Biochem. Parasitol. 64 (2), 337-340 (1994) MEDLINE 95021510 PUBMED 7935611 COMMENT Original Source text: Trypanosoma cruzi trypomastigote DNA. PEATURES 1. 1929 Source /organism="Trypanosoma cruzi" / Anol type="genomic DNA" / Ab xref="taxon:5693" / Ab xref="taxon:5693" / Ab xref="taxon:5693" / Codon_start=1 / product="trans-sialidase"	
GATTG GATTG CTGGA CTGGA CTGGA CTGGA CTGGA CTGGA		SCTCA SCTCA SGGGA ATCGA NTCGA INTCGA	CTGC 997 CTGC 1021 CTGC 1057 CTGC 1057 CTGC 1011 CTGC 1117 CAGTA 1141 CAGTA 1177	ACCAG 1237 IGATC 1261 CATC 1297 IGTG 1321
302 TTGCCATCAAGAACAGTCGTGCATCGTCTTTCTCGTGTGGTGGATCCCACAGTGATTG 318 TTGCCATCAAGAACAGTCGTGCATCGTCTTTTCTCGTGTGGTGGATCCCACAGTGATTG 320 TGAAGGCAACAAGCTTTACGTCCTGGTTGGAAGCTACAACAGTGATTG 321 TGAAGGCAACAAGCTTTACGTCCTGGTTGGAAGCTACAACAGTTCGAGGAGCTACTGGA 322 TGAAGGCAACAAGCTTTACGTCCTGGTTGGAAGCTACAATAGTTCGAGGAGCTACTGGA 422 CGTCGCATGGTGATGCGAGAACATGCGAAGTTGCTGGTGAGGAGCTACTGGAG 424 CGTCGCATGGTGATGCGAGAACATGCGAATTCTGCTTGCCGTTGGTGAAGTCACAAGAGTACAAGAGAGAAGTCACAAAGAGAAGTCACAAAGAGAAGAGAAGAGAAGAAGAAGAAGAAGAAGAAG	518 CCACTGGGGGGGGGGAAAAACTGCGAGTATCAAATGGGGGGGG			1178 ACGAGGTACAGCCTTGTTTTTGCGCGCCTGGTTGGCGACTACGGGTACGGGTACGGGTACGGGTTGAATCAGGTTGGGGCGCGACGATGGGTTGGGGCTACGGGTTGGGGTTGGGGTTGGGTTGGGAATCAGGAATCAGGAATCAGGAATCAGGAATCAGGAATTTGGGACCCTGTCCAGCATTTGCACCCCTGTCGTGGTTGGT
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93.9%; Score 1886.6;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1901; Conservative 0; Mismatches
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TCTTGAGCCAGGACCTGATTGGCACGGGAGCACATGGACAGCAGCAGCGACACGAGTG 1924				Db PAT 29-JAN-2003	qa a	<i>₹</i> 0 1	dairy source	े	1929; 0; Gabs	12					421				AGGTG	601 544 661	### 1929; 1929; 1929; 0, Gaps 0, Gaps 0, Gaps 1929; 1929; CCGCCCTTGTTA 121 CCGCCCTTGTTA 121 CCGCCCTTGTTA 131
	1982 AAAGA	o 1925 CCTGA 1929	2 LINS	AR261980	AR261980 AR261980.1	SM	Unclassified. I (bases 1 to 1929) Pelletier,M., Barker,W.A., Hakes,D.J. Methods for producing sialyloligosacch Patent: US 6323008-A 3 27-NOV-2001;	ES ource	<pre>y Match Local Similarity 98.3%; Score 1886.6; DB 6; Local Similarity 98.8%; Pred. No. 0; hes 1901; Conservative 0; Mismatches 24; I</pre>	62	122	182	242	302	362	422	4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5)	542	542 485 602	from patent US 6323008. GI:28073278 GI:28073278 GI:28073278 d. to 1929) L, Barker, W.A., Hakes, D.J. and Zopf, D.A. and
### AAAA 1986 ### AAAA 1986 ### AAAA 1986 ### AZ51980	### ### ### ### ### ### ### ### ### ##	MR261980	### ### ##############################	Unknown. Unknown. Unknown. Unknown. Unclassified. Unknown. Unclassified. Unknown. Unclassified. Unknown. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Loazion/Qualifiers Loazion/Qualifiers Angly Objectoring stayly oligosaccharides in a dairy source set of stayly oligosaccharides in a dairy source set oligosaccharide stayloligosaccharides stayloligos	Unknown. Unknown.	Unclassified. 1 (Dases I to 1229) Pelletar, M. A., Hakes, D. J. and Zopf, D. A. Methods for producing sialy/loligosaccharides in a dairy source Methods for producing sialy/loligosaccharides in a dairy source Methods for producing sialy/loligosaccharides in a dairy source Methods for producing sialy/loligosaccharides in a dairy source Methods for producing sialy/loligosaccharides in a dairy source 1	MONETON JOSEPH JULIANO MAINTENER JULIANO MAINTEN	destructive 93.94; Score 1886.6; DB 6; Length 1929; Best Local Similarity 98.84; Pred. No. 0; Ratches 1901; Conservative 0, Mismatches 24; Indels 0; Gaps 0; Ratches 1901; Conservative 0; Mismatches 24; Indels 0; Gaps 0; Indel [62 TGGCACCCGGATCGACCCGACTTGACCCGTTTAAGCGGCAAAGCTCCAAGGTCCCATTG 121 5 TGGCACCCGGATCGACGGTTGACCTTTTAAGCGGCAAAGCTCCCAAGGTCCCATTTG 121 65 AAAAGGACGGCAAAGCTCCCACCCGTCCCGCCCCCCCCCC	122 ANARGAGGGGAAAGTCACCGAGGGGTTGTCCACTCGTCCCCCCCC	182 ATTITITICGGGGGGGAAATGGGAAATGGGAAGCTGCTACGAAACATCCAATGACAACT 241 125 ATGTGGACGGGGGTGATGGCTGCCGCGCGCCTCGCTACGAAACATCCAATGACAACT 241 126 ATGTGGACGGGGGTGATGGTTGCCATCGCGGACGCTCGCAACACTCCAATGACAACT 241 127 CCCTCATTGATACGGTGGCAAGTACAGCGTGGACGACGTGGGAGACCCAAA 244 128 CCCTCATTGATACGGTGGCAAGTACAGCGTGGACGACGTGGAGAACACTCCAAA 244 129 TTGCCATCAAGAACAGTCGTGCATCGTTTCTCGTGTGGTGAACTCCAAGTGATTG 304 120 TTGCCATCAAGAACAGTCGTGCATCGTTTTCTCGTGTGGTGAATCCAAGTGATTG 304 121 TTGCCATCAAGAACAGTCGTGCATCGTTTTCTCGTGTGGTGAATCCAAGTGATTG 304 122 TGAAGGGCAACAAGATTACGTCCTGGTTTGCTGTTTCTCGTGTGGTGATCCAAGTATTG 304 123 TGAAGGGCAACAAGATTACGTCCTGGTTTGCTTTTCTCGTGTGGTGATTCGAAGTATTG 304 124 TGCCATCGCGACGAAGAACTGCGATATTCTGCTGTTCGTGGAGGTCACTGAAGT 424 125 CCACTGCGGGCGCAAGATAACTGCGAATATTCTGCTGGTGGTCACTGAAGG 484 126 CCACTGCGGGCGCAAGATAACTGCGAATATCAATCGGGGAGCCCCGTGTCACTGAAGG 484 127 CCACTGCGGGCGCAAGATAACTGCGAATATCAATCGGGGACCCCGTGTCACTGAAGG 484 128 CCACTGCGGGCGCAAGATAACTGCGAATATCAATCGGGGACCCCGTGTCACTGAAGG 484 129 CCACTGCGGGCGCAAGATAACTGCGAATATCAATCGGGGACCCCCTGTCACGGGG 691 129 AATTTTTCCGGCGGCAAAATGGAAGGAATCCACAAATCAATTTCTTGGCGGTGCACTGAAGG 691 120 TTGCCAATTGTGGCGAAATGGAAATCGAACACAAATCAATTTCTTGGCGGTGCACTGAAGG 691 120 TTGCCAATTGTGGCGTAAATGGAAATCCAAATCAATTTCTTGGCGGTGCAGGTG 601 120 TTGCCAATTGTGGCGTAAATGGAAATCCAAATCAATTTCTTGGCGGTGCAGGTG 601 120 TTGCCAATTGTGGCGTCCAACGGGAAATCTTGTGTGAACAAAAAAACAATCAAATCAAATCAATTCTTTGGCGGTGCAAGATGAAAACAACACACAAATCAATC	242 CCCTCATTGATACGGGGGGGGGGGGGGGGGGGGGGGGGG	183 CCLICATION COLOR AND AND AND AND AND AND AND AND AND AND	362 TGAAGGGCAACAAGCTTTACCTCCGGTTGGAAGCTACACACTTCGAGGGCTACTGGA 421 305 TGAAGGGCAACAACACTTTACCTCCTGGTTGGAAGCTACTCGAGGGCTACTGGA 364 422 CGTCGCATGGTGATGCTGGAAGTTTCTGCTTGCTGGTGAGGTCACTGGA 364 422 CGTCGCATGGTGATGCGAGACTGGGATATTCTGCTTGCTT	422 CGTCGCATGGTGATGCGAGAGTATTCTGCTTGCCGTCGGTCACGAAGT 481 [425 CCACTGCGGGCGCAAGATAACTGCGAGTATCAAATGGGGGAGCCCCGTGTGAAGG 541	542 ANTITITICCGGGGGAATGGAAGGATGCACACAATCATTTCTTGGCGGTGCAGTG 601 485 ANTITITICCGGGGAAATGGAAGGATGCACACACAATTACTTTGCGGTGCAGGTG 504 602 TTGCCATTGTGGCGTCCAACGGGAATCTTGTTGTGTGCGGTTACGAACAAAAGA 661	485 AATTITICCGGGGGAAANGGAAGGCACACACACATITICITGGGGGGGGGGGGGGGGG	545 Trgccatrgredecrecaaceeeaarcrrerererererererereaaaaaaa 604		

JOURNAL Gene 160 (1), 123-128 (1995) MEDLINE 9535443 FEATURES Location/Qualifiers Location_Qualifiers Location_Coulifiers Location_Coulifiers Location_Coulifiers Apperature	Query Match Best Local Similarity 98.4%; Score 1877; DB 3; Length 1929; Best Local Similarity 98.4%; Pred. No. 0; Matches 1895; Conservative 0; Mismatches 30; Indels 0; Gaps 62 TGGCACCCGGATCGAGCGGTTGAGCTGTTTAAGCGGCAAAGCTCGAAGGTGCCATTTG [Qy 422 CGTCGCATGGTGATGATTGTCGTTGGTGAGGTCACGAAGT 481
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FEATURES

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Submitted (20-JUN-2002) Microbiologia Imunologia e Parasitologia,
Universidade Federal de Sao Paulo - UNIFESP/EPM, Botucatu 862, Sao
Paulo, SP 04023-062, Brasil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (44031. .>4885)
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Kelly, J.M. and Franco da Silveira, J.
                                                                                                                                                                                                                                                                                              organism="Trypanosoma cruzi"
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Qy 1882 TACAACCGTCAGTGATGCCGAGGAGTCTTGTTCTTGAGCCAGGACCTGATT 1941 Db 23361 TACAACCGTCAGCTGAATGCCGAGGAGTACCAGACCTTGTTTCTTGAGCCAGGACCTGATT 23302 Qy 1942 GGCACGGAAGCACACATGGCAGCAGCAGCGGAGCATGAAGAAGAAGTAGCCCGGATC 2000 Db 23301 GGCACGGGAAGCACATGGGCAGAGAGCAGCAGCAGCAGCACACACA	RESULT 10 TCR276679 LOCUS LOCUS DEFINITION Trypanosoma cruzi TCTS gene for trans-sialidase. VPRSTON A171670 A171670 A171670	_		JOURNAL Submitted (10-MAR-2000) Laroy W.H.M., Department of Molecular Biology, Ghent University and VIB, K.L. Ledeganckstraat 35, B-9000, BELGIUM REWARK Revised by author 21-SEP-2000 FEATURES Location/Qualifiers source 1. 1932	/organism="Trypanosoma cruzi" /mol_type="genomic DNA" /strain="Y=strain" /db_xref="taxon:5693" /dev_stage="trypomastigote" /qene="Trypomastigote"	ransfer of sialic acids among glyc=1 ans-sialidase" (ARC34453.1" 1.337476" TREMBL:09BHJS"	USYWAYALADAXY DISNINSKI IDTYAKXS DUDGETWETOLA KUSRVG VKGWLYVLVGSYYS SRSYWSHGDARDWDILLAVGEVTKSI TAGGKI LKKFFPAEMEGWHTNOFLGGAGAVALYASNGNILVYPVQYTKKRQVES WKFGKGRSDFGCSEPVALEWEGKLI INTRVDWKRRLVYESSDMGNTW GPSFKSDHFGSQSETAVIL TEGRRWALFTHPLNFKRRWLRDRLINLW VSIGDENSY SSYLYKDDKYCLHEINTDEVYSLYFARLVGELR ITR HLSSICTPADPAASSSEGGCBAVTTVGLVGFLGGARSQNVWEDAR R VRNGIKKAGVGGGALWPVSQQGQNQRYRFANHAFTLVASVTIHEAPR SSGGKKLLGLSYDEKHQWQPIYGSFPYTPTGSWETGRRYHVYLTVAN LEGGGOTVVPDGRTPDISHFYVGGYGRSDMPTISHVTVNIVLLYNRQ SQDLIGTEAHNDSSSDTSA"	Query Match 88.7%; Score 1782.4; DB 3; Length 1932; Best Local Similarity 95.6%; Pred. No. 0; No. 0; Matches 1844; Conservative 0; Mismatches 81; Indels 3; Gaps 1; QY 62 TGGCACCCGGATCGAGCTGAGTTTAAGCGGCAAAGCTCGAAGATTG 121

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Frasch, A.C.C.
Direct Submission
Submitted (21-JAN-1991) A.C.C. Frasch, Fundacion Campomar, Av
Patricias Argentinas 435, 1405 Buenos Aires, Argentina, South
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                                    TGTGGTCCCGCTGTCACCACGGTTGGTCTTG
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
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T.cruzi shed-acute-phase-antigen (SAPA) gene.
X57235 S65039
Shodya 21:10943
Shed-acute-phase-antigen.
                                       ATCCAGCCGCTTCGTCGTCAGAGCGTGGT
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2133 bp DNA linear INV 06-SEP-1999 cruzi trans-sialidase gene, clone 199, 5'-region.
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trans-sialidase of Trypanosoma cruzi: location of galactose-binding
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CTTCTGGTGGCAAAAACTCCTGGGGCTCTCGTACGACGAGA
     AGCACCAGTGGCAGCCAATATACGGATCAACGCCGGTGACGCCGACCGGATCGTGGGAA
                                          1682 TOGGTAAGAGGTACCACGTGGTTCTTACGATGGCGAATAAAATTGGTTCGGTGTACATTG
                                                                                                                                                                                                            TCTCCCACTTCTACGTTGGCGGGTATGGAAGGAGTGATATGCCAACCATAAGCCACGTGA
                                                                                                                                                  CGGTGAATAATGTTCTTCTTTACAACCGTCAGCTGAATGCCGAGGAGATCAGGACCTTGT
                                                                                                                                                                                    The Trypanosoma cruzi neuraminidase contains sequences similar bacterial neuraminidases, YWTD repeats of the low density lipoprotein receptor, and type III modules of fibronectin 5.Exp. Med. 174 (1), 179-191 (1991)
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Prioli,R.P.
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Trypanosoma cruzi
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
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Submitted (26-NOV-1997) Chuenkova M.
University of Bath, University of bath
BA2 7AY, UNITED KINGDOM
Location/Qualifiers
1. 2133
/organism="Trypanosoma cruz:
/mol type="genomic DNA"
/strain="Silvio X-10/4"
/db_xref="taxon:5693"
/clone="19y"
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                                             CCACTGCGGGCGGCAAGATAACTGCGAGTATCAAATGGGGGAGCCCCGTGTCACTGAAGG
                                                                   AATTITITCCCGGCGGAAATGGAAGGAATGCACAAATCAATTTCTTGGCGGTGCAGGTG
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                                                                                                                                                                                                                                                                                                                                                                          al source text: T.cruzi (strain Silvio) DNA, clone 7F.
Location/Qualifiers
1. .5403
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neuraminidase.

Trypanosoma cruzi

Trypanosoma cruzi

Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma; Schizotrypanum.

I (bases I to 5403)

Pereira,M.E., Mejla,J.S., Ortega-Barria,E., Matzilevich,D.;
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Best Local Similarity 93.3%; Pred. No. 0;
Matches 1852; Conservative 0; Mismatches 123; Indels 10;
                                           5403 bp DNA lines (TCNA) gene, complete cds.
                                                         .cruzi neuraminidase
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VERSION
KEYWORDS
SOURCE
ORGANISM
RESULT 13
TRBTCNAA
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AUTHORS
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Ubmura,H.
Direct Submission
Submitted (27-MAY-1995) Haruki Ubmura, Nagasaki University,
Submitted (27-MAY-1995) Haruki 1-12-4 Sakamoto, Nagasaki, Nagasaki
Institute of Tropical Medicine; 1-12-4 Sakamoto, Nagasaki, Nagasaki
852, Japan (E-mail:H-Ubmura@cc.nagasaki-u.ac.jp,
751:81-958-49-7837, Rax:81-958-49-7805)
Tel:81-958-49-7837, Rax:81-958-49-7805
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                                                                                                                                                                                                                                                                                        /gene="TCTS-193"
1. ..>2100
/g.n.=TCTS-193"
/function="one of the trans-sialidase gene family"
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Pred. No. 0;
0; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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                                                                                                                                                                    /organism="Trypanosoma cr
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ilarity 91.7%;
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Trypanosoma cruzi TCTS-193 gene for trans-sialidase homolog,
partial cds.
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Isolation and expression of an open reading frame encoding stalidase from Trypanosoma rangeli
Mol. Blochem. Parasitol. 79 (1), 21-33 (1996)
97001677
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
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Briones, M.R., Egima, C.M., Eichinger, D. and Schenkman, S.
Trans-stalldase genes expressed in mammalian forms of Trypanosoma cruzi evolved from ancestor genes expressed in insect forms of the
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Submitted (27-AUG-1993) Marcelo Briones, Bscola Paulista de
Medicina, Microbiologia, Imuno e Parasitologia, Rua Botucatu, 862,
8 andar, Sao Paulo, Sao Paulo, Brazil, 04023-062
On Jan 18, 1995 this sequence version replaced gi:430944.
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                                      TGGGTAAGAGGTACCACGTGGTTCTTACGATGGCGAATAAAATTGGTTCGGTGTACATTG
                                                  TCTCCCACTTCTACGTTGGCGGGTATGGAAGGAGTGATATGCCAAACCATAAGCCACGTGA
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Evikaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma; Schlzotrypanum.
E 1 (bases 1 to 2749)
S Briones, M.R., Egima, C.M. and Schenkman, S.
Trypanosoma cruzi trans sialidase gene lacking C-terminal re and expressed in epimastigote forms
Mol. Blochem. Parasitol. 70 (1-2), 9-17 (1995)
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protein id="AAC98544.1"
db xref="C1:624626"
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	SUMMARIES	Description	ABA98876 Aba98876 Plasmid e	ADD06429 Add06429 DNA encod	AAX26611 AAX26611 Trypanoso	AAX26612 Alpha (2-3	ADC21500 T. cruzi	ADC21532 T. cruzi	AAQ49594 Encodes p					AAZ29719 Aaz29719 T. cruzi	AAT69167 Aat69167 Trypanoso	AAX81756 DNA encod	ABV74081 Abv74081 DNA encod	AAD16128 Aad16128 Hexa-His-	AAZ38274 Human tyr	AAZ50043 Aaz50043 DNA encod	AAS00250 LFn-Bcl-X	AAA49432 Aaa49432 Neisseria	AAZ50042 Aaz50042 DNA encod	ADC19976 Adc19976 pET-28a-c
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The invention relates to a composition useful for treating or preventing mycoplasma infection in a subject suffering from a disorder characterised CC by increased cell proliferation or by co-infection with a second microbe, compositions an agent that prevents or inhibits shalls caid-mediated compositions of the invention may be described as; antiatherosclerotic, compositions are useful to treat diseases associated with undesirable antibacterial, antiviral, anti-HIV, cytostatic and vasotropic. The compositions are useful to treat diseases associated with undesirable malignancy, by reducing or preventing mycoplasma infection. Examples of colon cancer, lung cancer and leukaemia. They are also useful to treat diseases associated with infection with other infections organisms colon cancer, lung cancer and leukaemia. They are also useful to treat septically human immunodeficiency virus or chlamydia species. They can be used to treat such diseases in humans or other animals, and con be administered in conjunction with conventional agents e.g. anti-colon cancer in conjunction with conventional agents e.g. anti-colon cancer in conjunction with conventional agents e.g. anti-colon cancer in cantuctic agents. The current sequence represents the xxx plasmid encoding the catalytic trans-sialidase unit of T. cruzi Fig 25; 63pp; English Claim 12; &\$66666666666666666666666666666666666

Sequence 2010 BP; 456 A; 488 C; 624 G; 442 T; 0 U; 0 Other;

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construction and a second microbe. Mycoplasmas are parasites of the respiratory epithelium and urogenital tract. Infections are typically segment to be co-factors in diseases such as AIDS and in sequelae after mycoplasma infections having an autoimmune basis. The agent prevents or inhibits sialic acid-mediated attachment of mycoplasma or co-cells of the subject and is an antibiotic or an enzyme having an carivity consisting of neuraminidase and/or trans-sialidase activity. The enzyme is derived from a Trypanosoma cruzi microorganism, where the caryme is antive or a recombinant enzyme. Results showed that trans-cary mycoplasmas from the neoplastic cells leading to their apoptosis. The composition or the agent that prevents or inhibits mycoplasma infection is useful for manufacturing a medicament for treating or preventing a disorder associated with increased cell proliferation, e.g. atherosclerotic vascular disease or malignant disease (tumour), or a disease associated with co-infection with mycoplasma and a second microbe such as human immunodeficiency virus or a Chlamydia microbe. The sequence
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                                                                                                                                                                         an agent that prevents or inhibits Mycoplasma infection, for
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03-JUL-2001; 2001BR-00002648.
03-JUL-2001; 2001WO-BR000083.
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Best Local Similarity
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The present sequence encodes Trypanosoma cruzi alpha(2-3) trans-
staldase. The protein is used in the method of the invention to produce
staldase. The protein is used in the method of the invention to produce
staly1-oligosaccharides, particularly staly1lactose, which are produced
by treating a dairy source such as a cheese processing waste strain with
an alpha (2-3) trans-staldase. The method can be used for producing
staly1-oligosaccharides, such as (2-3)sialy1lactose for pharmaceutical
use. (2-3)staly1lactose has been shown to neutralise enterotoxins of
various pathogenic microbes including E. coli, vibrio cholerae and
(alpha-Neu3A-(2-3)-Gal-beta-(1-4)-GlC) interferes with colonisation of
telicobacter pylori and thereby prevents or inhibits gastric and duodenal
ulcers. (2-3)staly1lactose has additionally been proposed to inhibit
immune complex formation by disrupting occupancy of the Fc carbohydrate
binding site on IgG and to be useful in treating arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Production of sialyl-oligosaccharides, particularly sialyl-lactose - by treating a dairy source such as a cheese processing waste stream with an alpha (2-3) trans-sialidase.
ACGGTGAATAATGTTCTTTTACAACCGTCAGCTGAATGCCGAGGAGATCAGGACCTTG
                                                                                                                                                                    TTCTTGAGCCAGGACCTGATTGGCACGGAAGCACACATGGGCAGCAGCAGCAGCAGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alpha(2-3) trans-sialidase; sialy1-oligosaccharide; sialyllactose; cheese processing waste strain; (2-3) sialyllactose; gastric ulcer; duodenal ulcer; arthritis; enterotoxin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trypanosoma cruzi alpha(2-3) trans-sialidase nucleotide sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAAGAAGTACGCCCGGATCCGGCTGCTAA 2010
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cheese processing waste strain; (2-3)sialyllactose; gastric ulcer; duodenal ulcer; arthritis; enterotoxin; ss.
                                                     (NEOS-) NEOSE TECHNOLOGIES INC
                                                                      1999-190079/16
processing
                                                                         P-PSDB; AAY01541.
                    WO9908511-A1
                                             14-AUG-1997;
                                                             Pelletier M,
            Тгураповоша
                             25-FEB-1999
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Hakes DJ,

Barker WA,

97US-00911393. 98WO-US016756

The present sequence encodes a functional Trypanosoma cruzi alpha(2-3) trans-sialidase which lacks amino acid repeats. The protein is used in the method of the invention to produce siallyl-oligosaccharides, particularly sialyllactose, which are produced by treating a dairy source such as a cheese processing waste strain with an alpha (2-3) transsialidase. The method can be used for producing sialyl-oligosaccharides, such as (2-3) sialyllactose for pharmaceutical luse. (2-3) sialyllactose for pharmaceutical luse. (2-3) sialyllactose including E. coli, vibrio cholerae and Salmonella. It has also been shown that alpha(2-3) sialyllactose (alpha-Neu5Ac-(2-3)-Gal-beta-(1-4)-Glc) interferes with colonisation of Helicobacter pylori and thereby prevents or inhibits gastric and duodenal ulcers. (2-3) sialyllactose has adductionally been proposed to inhibit immune complex formation by conserved. Production of sialyl-oligosaccharides, particularly sialyl-lactose - by treating a dairy source such as a cheese processing waste stream with an alpha (2-3) trans-sialidase. Sequence 1929 BP; 442 A; 463 C; 590 G; 434 T; 0 U; 0 Other; Disclosure, Fig 3; 84pp; English. useful in treating arthritis

122 AAAAGGGGGGCAAAAGTCACCGAGGGGGTTGTCCAGTTGGTTCCGGCCTTCTTA 181 241 244 361 64 304 421 TGGCACCCGGATCGAGCCGAGTTGAGCTGTTTAAGCGGCAAAAGCTCGAAGGTGCCATTTG TGGCACCCGGATAGAGCCGAGTTGAGCTGTTTAAGCGGCAAAGCTCGAAGGTGCCATTTG ATGTGGACGGGTGATGGTTGCCATCGCGACGCTCGCTACGAAACATCCAATGACAACT CCCTCATTGATACGGTGGCGAAGTACAGCGTGGACGATGGGGAGACGTGGGAGACCCAAA CCCTCATTGATACGGTGGCGAAGTACAGCGTGGACGATGGGGAGACGTGGGAAACCAAA TTGCCATCAAGAACAGTCGTGCATCGTCTTTCTCGTGGTGGATCCCACAGTGATTG TGAAGGCCAACAAGCTTTACGTCCTGGTTGGAAGCTACAACAGTTCGAGGAGCTACTGGA Gaps Score 1875.4; DB 2; Length 1929; Pred. No. 0; 0; Mismatches 31; Indels 0; Query Match
Best Local Similarity 98.4%;
Matches 1894; Conservative (182 242 185 302 245 362

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364

CGTCGCATGGTGATGCGAGAGACTGGGATATTCTGCTTGCCGTTGGTGAGGTCACGAAGT 481

422

1021 1024 1201 601 724 TGACGGATAACCAGCGCATTTATAACGTTGGGCAAGTATCCATTGGTGATGAAAATTCCG 1081 1084 1085 ACGAGGTGTACACCTTGTTTTTGCGCGCCTGGTTGGCGAGCTACGGATCATTAAATCAG 1144 1261 1204 1321 1264 1381 1324 1441 661 604 721 664 781 841 784 901 844 961 904 1384 1501 CGTTCACGCTGGTGGCGTCGGTGACGATTCCGAGGTTCCGAGGGTCGCGAGTCCTTTGC 1561 964 1444 AATTTITCCCGGCGGAAATGGAAGGAATGCACAAATCAATTTCTTGGCGGTGCAGGTG CCACTGCGGGCGGCAAGATAACTGCGAGTATCAAATGGGGGAGCCCCGTGTCACTGAAGG TTGCCATTGTGGCGTCCAACGGGAATCTTGTGTACCCTGTGCAGGTTACGAACAAAAGA AGCAAGTTTTTTCCAAGATCTTCTACTCGGAAGACGAGGGCAAGACGTGGAAGTTTGGGG TTGCCATTGTGGCGTCCAACGGGAATCTTGTGTACCCTGTGCAGGTTACGAACAAAAGA TCATAAACACTCGAGTTGACTATCGCCGCCGTCTGGTGTACGAGTCCAGTGACATGGGGA ATTCGTGGGTGGAGGCTGTCGGCACGCTCTCACGTGTGGGGGCCCCTCACCAAAATCGA 902 ACCAGCCCGGCAGTCAGAGCTGCTGCCGTGACCATCGAGGAATGCGTGTTATGC CCTACAGCTCCGTCCTGTACAAGGATGATAAGCTGTACTGTTTGCATGAGATCAACAGTA 1142 ACGAGGTGTACAGCCTTGTTTTGCGCCCTGGTTGGCGAGCTACGGATCATTAAATCAG TGCTGCAGTCCTGGAAGAATTGGGACAGCCACCTGTCCAGCATTTGCACCCTGCTGATC 1145 TGCTGCAGTCCTGGAAGAATTGGGACAGCCACTGTCCAGCATTGCAGCATGTGATC GCTTTTGTCGCACAGTGCCACCAAAACCGAATGGGAGGATGCGTACCGCTGCGTCAACG CAAGCACGCAAAATGCGGAGAGGGTTCCGAACGCTTTGAAGTTTGCGGGGGTTGCCGAG GGGCGCTTTGGCCGGTGAGCCAGCGGGCAGAATCAACGGTATCACTTTGCAAACCACG 425 365 482 542 485 842 602 545 662 605 665 725 722 782 785 962 1022 1082 1025 965 1202 1262 1205 1322 1265 1382 1325 1442 1502 g ሯ ŝ 셤 δ 셤 δ a ò 셤 a ઠે Š 셤 ò a 셤 ઠે ò 원 장 g 8 셤 ò g ઠે a ઠે ద ò 셤 à 셤 ò

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condition selected from: Transmission included and an interleukin-6 (IL-6) secretion inducing peptide appearing as ADC21513 or ADC21511 called C44 and C14, or its variant, and an interleukin-6 (IL-6) secretion inducing peptide appearing as ADC21513 called TR-1 (terminal repeat 1). Also peptide are a composition comprising the peptides, fusion protein comprising the peptides, fusion partient protein and a physiological acceptable carrier, providing trophic support for neurons or glial cells in a mammal (comprising a therapeutically effective amount of T. cruzi transcally effective amount of T. cruzi transcallidase (TS) or a neurotrophic variant) and stimulating (M3) the secretion of IL-6 (interleukin-6) in a mammal comprising administering TS or an IL-6 inducing variant. The fusion partner comprises a mammalian corresponded for the condition selected from: amyotrophic lateral sclerosis, Alzheimer's disease, parkinson's disease, parkinson's disease, (LIP). The peptides are useful in providing trophic support for neurons and glial cells in a mammal suffering a condition selected from: amyotrophic lateral sclerosis, Alzheimer's disease, parkinson's disease, (Abagas' Ghagas' Ghagas' Ghagas' Ghagas' Ghagas' Ghagas' Ghagas' Ghagas' Ghagas' Ghagas' Ghagas' Ghagas' Compandant of IL-6. The present sequence encodes trans sialidase clone to be a condition of IL-6. The present sequence encodes trans sialidase clone
                                                                                                                                                                                                                                                                        T. cruzi trans-sialidase derived neurotrophic and interleukin-6 secretion inducing peptides, useful in the treatment of neuronal degeneration caused for example by Chagas' disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2133 BP; 485 A; 529 C; 635 G; 484 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1753.8; DB 9; Length
Pred. No. 0;
0; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 1; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                             relates to a T.
99US-0172881P
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Matches 1831; Conservative
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                                                                                                                         Pereira
                                                                                                                                                                                     WPI; 2003-786654/74.
                                                            (TUFT ) UNIV TUFTS.
                                                                                                                                                                                                                  P-PSDB; ADC21501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
   20-DEC-1999;
                                                                                                                         Chuenkova M,
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                                                                                                                                                                                                                     GGCACCAGTGGCAGCCAATATACGGATCAACGCCGGTGACGCCGACCGGATCGTGGGA
                                                                                               TGGGGCGCGGAGCTCTTCTGGTGGCAAAAAACTCCTGGGGGCTCTCGTACGACGAGA
                                                                                                                                                                                     1622 AGCACCAGTGGCAGCCAATATACGGATCAACGCCGGTGACGCCGACCGGATCGTGGGAGA
                                                                                                                                                                                                                                                                                                              TGGGTAAGAGGTACCACGTGGTTCTTACGATGGCGAATAAAATTGGTTCGGTGTACATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T. cruzi trans-sialidase gene, TS, clone 19Y.
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Trans-stalidase; gene; TS; ds; neurotrophic peptide; interleukin-6; IL-6 secretion inducing peptide; neuron; glial cell; trophic support; clilary neurotrophic factor; CNTF; leukaemia inhibitory factor; LIF; amyotrophic lateral sclerosis; Albheimer; s disease, Parkinson's disease; Huntington's disease; Chagas' disease; peripheral neuropathy; palsy; multiple sclerosis; stroke; brain trauma; spinal cord trauma;
                        ATATACGGATCAACGCCGGTGACGCCGACCGGATCGTGGGGATGGGTAAGAGGTACCAC
                                                                                 GTGGTTCTTACGATGGCGAATAAAATTGGTTCGGTGTACATTGATGGAGAACCTCTGGAG
                                                                                             TIGGTICTIACGATGGCGAATAAATTGGCTCCGTGTACATTGATGGAGAACTTCTGGAG
                                                                                                                   GGTTCAGGGCAGACCGTTGTGCCAGACGGAGGACGCCTGACATTCTCCCACTTCTACGTT
              TCTTCTGGTGGCAAAAACTCCTGGGGCTCTCGTACGACGAGAAGCACCAGTGGCAGCCA
                                                                                                                             GGCGGGTATGGAAGGAGTGATATGCCAACCATAAGCCACGTGACGGTGAATAATGTTCTT
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/product= "Trans-sialidase"
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                              IGTGTACCCTGTGCAGGTTACGAACAAAAAGAAGCAAGTTTTTCCAAG
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T. cruzi trans-sialidase derived neurotrophic and interleukin-6 secretion inducing peptides, useful in the treatment of neuronal degeneration caused for example by Chagas' disease.

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Query Match 85.0%; Score 1708.2; DB 9; Length 5403; Best Local Similarity 93.3%; Pred. No. 0; Matches 1852; Conservative 0; Mismatches 123; Indels 10; Gaps Sequence 5403 BP; 1092 A; 1599 C; 1479 G; 1233 T; 0 U; 0 Other; 308 139 427 199 259 319 379 667 439 499 487 547 607 727 ઠે 유 ઠ a δ d ઠે a ò 셤 ò 셤 ò 셤 ઠે g ò g

GAGCGTGGTTGTGGGTCCCGCTGTCACCACGGTTGGTCTTGTTGGCTTTTTTGTCGCAGT 1338 GAGAGGGTTCCGAACGGTTTGAAGTTTGCGGGGGTTGGCGGAGGGGCGCCTTTGGCCGGTG 1458 TCGCTGACGATTCACGAGGTTCCGAGCGTCGCGAGTCCTTTGCTGGGTGCGAGCCTGGAC 1578 ATATACGGATCAACGCCGGTGACGCCGACCGGATCGTGGGAGATGGGTAAGAGGTACCAC 1698 ATATACGGATCAACGCCGGTGACGCCGACGGATCGTGGGAGACGGGTAAAAGGTACCAC 1983 GGCTGCTCTGAACCTGTGGCCCTTGAGTGGGAGGGGAAGCTCATCATAAACACCCGAGTT GTCGGAACCGTCTCGCGTGTGTGTGGGGCCCCTCACCAAAATCGAACCAGCCCGGCAGTCAG AATTTTAAGGGAAGGTGGCTGCCCGACCGACTGAACCTCTGGCTGACGGATAACCAGCGC ATTTATAACGTTGGGCAAGTATCCATTGGTGATGAAAATTCCGCCTACAGCTCCGTCCTG AGCCAGCAGGGCAGAATCAACGGTATCACTTTGCAAACCACGCGTTCACGCTGGTGGCG TCGGTGACGATTCACGAGGCTCCGAGGCCCGCGAGTCCCTTGCTGGGTGCGAGCCTGGAC GIGGTICTIACGAIGGCGAATAAAATIGGTICGGIGTACATIGAIGGAGAACCICTGGAG GTCGCCACGCTCTCACGTGTGTGGGGCCCCTCACCAAAATCGAACCAGCCCGGCAGTCAG AGCAGCTTCACTGCCGTGACCATCGAGGGAATGCGTGTTATGCTCTTCACACACCCGCTG ATTTATAACGTTGGGCAAGTATCCATTGGTGATGAAAATTCCGCCTACAGCTCCGTCCTG GTTTTTGCGCGCCTGGTTGCCGAGCTACGGATCATTAAATCAGTGCTGCAGTCCTGGAAG GCCACCAAAACCGAATGGGAGGATGCGTAACCGCTGCGTCAACGCAAGCACGGCAAATGCG AGCCAGCAGGGGCAGAATCAGCGTATCGTTTTGCAAACCACGCGTTCACGCTGGGGGCG retreregegeaaaaacrecregegereregrandaacaacaacaagaageaacaa GGCTGCTCTGAACCTGTGGCCCTTGAGTGGGAGGGGAAGCTCATCATAAACACTCGAGTT TACAAGGATGATAAGCTGTACTGTTTGCATGAGATCAACAGTAACGAGGTGTACAGCCTT AATTGGGACAGCCACCTGTCCAGCATTTGCACCCCTGCTGATCCAGCCGCTTCGTCGTCA GAGAGGETTCGGAACGETTTGAAGTTTGCGGGGGTTGGCCGAGGAGCGCTTTTGGCCGGTG TCTTCTGGTGGCAAAAACTCCTGGGGCTCTCGTACGACGAGAAGCACCAGTGGCAGCA 1027 979 1447 1507 296 1087 1147 1207 1267 1039 1327 1099 1387 1159 1566 1339 1625 1399 1684 1459 1804 1579 1864 1639 1924 799 859 919 1279 1699 739 1219 1744 1519 8 8 셤 엄 g g g 8 8 8 g 요 Š ò ઠે δ 셤 8 ò g ઠે 8 ò જે 셤 à à 셤 ઠે g ò 셤 δ 원 ઠ comprising the peptide appearing as ADC21513 or ADC21511 or ADC2151 or A CTTCTTGCGATCTGCCCCAGCGAGCCCGCGTACGCCCTGGCACCCGGATCGAGCCGA 367 138 426 198 546 318 486 258 909 378 999 438 726 498 786 558 846 618 996 GTTGAG-GGTTTAAGCGTAAGAATTCGACGGTGCCGTTTGAAGACAAGGCCGGCAAAGTC ACCGAGCGGGTTGTCCCTTCCCCTTCCCCCTTGTTAATGTGGACGGGGTGATG GTTGCCATCGCGGACGCTCGCTACGAAACATCCAATGACAACTCCCTCATTGATACGGTG GTTGCCATCGCGGACGCTCGCTACGAAACATCCAGTGAAAACTCCCTCATTGATACGGTG GCGAAGTACAGCGTGGACGATGGGGAGACGTGGGAGACCCAAATTGCCATCAAGAACAGT GCGAAGTACAGCGTGGACGATGGGGAGACGTGGGAGACCCCAAATTGCCATCAAGAACAGC CGTGTATCGTCTGTTTCTCGTGTGGTGGTCCCACCGTGATTGTGAAGGGCAACAAGCTT TACGTCCTGGTTGGAAGCTACAACAGTTCGAGGAGCTACTGGACGTCGCATGGTGATGCG TACGTCCTGGTTGGAAGCTACTATAGTTCGAGAAGCTACTGGTCGTCGCATGGTGATGCG ATAACTGCGAGTATCAAATGGGGGGGGCCCCGTGTCACTGAAGGAATTTTTCCCGGCGGAA ATGGAAGGCATGCACAAATCAATTTCTTGGCGGCGGGGGTGTTGCCATTGTAGCGTCC CATCATCACAGCGGCGTGCCGCGCGCGCCATATGGCACCCGGATCGAGCCGA GTTGAGCTGTTTAAGCGGCAAAGCTCGAAGGTGCCATTTGAA---AAGGGCGGCAAAGTC CGTGCATCGTCTTTCTCGTGTGGTGGATCCCACAGTGATTGTGAAGGGCAACAAGCTT **ATGGAAGGAATGCACACAAATCAATTTCTTGGCGGTGCAGGTGTTGCCATTGTGGCGTCC** invention relates to a T. cruzi trans-sialidase (TS) derived 33; 79pp; English 2 Ω 787 559 907 619

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1033 CAGCGCATTTATAACGTTGGGCAAGTATCCATTGGTGATGAAAATTCCGCCTACAGCTCC 1092
                                                                                          241 GAGGCTGTCGGCACGCTCTCACGTGTGTGGGGCCCCTCACCAAAATCGAACCAGCCCGGC 300
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26-APR-1994
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10-NOV-1992;
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                                                                                                                                                      CTTTACAACCGACGACAGGTGAATACCGAGGAGTCAGGACCTTGTTCTTGAGCCAGGAC 2223
                                                                                                                                                                                                                      This is the nucleotide seguence of the portion of trans-sialidase which imparts trans-sialidase and/or neuramidase activity. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New trans-sialidase polypeptide(s) isolated from Trypanosoma - used for transferring sialic acid or for treating or preventing trypomastigote infection.
CTTTACAAC - - CGTCAGCTGAATGCCGAGGAGATCAGGACCTTGTTGAGCCAGGAC
                                                                                                                                                                                                     CTGATTGGCACCGAAAGCACACATGGGCAGCAGCAGCAGCAGCAGTGAAAGAAGTACGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Encodes protein with trans-sialidase and/or neuramidase activity.
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Chagas' Disease; parasite; ss.
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(first entry)
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P-PSDB; AAR42014.
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26-APR-1994
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10-NOV-1992;
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Trypanosome; trans-sialidase; neuramidase; sleeping sickness;
Chagas' Disease; parasite; ss.
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                                                                                                                                                                     Clone 154 encoding trans-sialidase gene active portion.
                                                                                                                                                                                                                                                                                                                                                                                 1. .494
/*tag= a
/note= "has trans-sialidase activity"
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Gaps

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CCGCTGAATTTTAAGGGAAGGTGGCTGCGCGACCGACTGAACCTCTGGCTGACGGATAAC 1032
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                                                                                                                                                                                                                                                                                                                                                                                                                  Clones 121 and 151, isolated from T.cruzi DNA library by homology to known neuramidase sequences, were found to have identical sequences in the region of the trans-sialidase gene necessary for enzymatic activity. The 121/151 nucleotide sequence (AAQ4955) is similar to the known TCNA sequence (AAQ49556) but distinct from the sequence of clone 154 (AAQ49597). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                           New trans-sialidase polypeptide(s) isolated from Trypanosoma - used fo
transferring sialic acid or for treating or preventing trypomastigote
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Pred. No. 2.8e-138;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                     Vandekerckhove
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                                                       trans-sialidase activity"
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 Location/Qualifiers
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                                                                                                              Clones 121 and 151, isolated from T.cruzi DNA library by homology to known neuramidase sequences, were found to have identical sequences in the region of the trans-sialidase gene necessary for enzymatic activity. The 121/151 nucleotide sequence (AAQ49555) is similar to the known TCNA sequence (AAQ49596) but distinct from the sequence of clone 154 (AAQ49597). (Updated on 25-MAR-2003 to correct PN field.)
                             for
                          New trans-sialidase polypeptide(s) isolated from Trypanosoma - used for transferring sialic acid or for treating or preventing trypomastigote
                                                                                                                                                                                                                                                                                                                  613 GCGTCCAACGGGAATCTTGTGTACCCTGTGCAGGTTACGAACAAAAAGAAGCAAGTTTTT
                                                                                                                                                                                                                                                                                                                                    GATTTTGGCTGCTCTGAACCTGTGGCCCTTGAGTGGGAGGGGAAGCTCATCATAAACACT
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                                                                                                                                                                                                                                                                                                                                                                           TCCAAGATCTTCTACTCGGAAGACGAGGCCAAGACGTGGAAGTTTGGGGAGGGTAGGAGT
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                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                     24.8%; Score 498.4; DB 2; Length 500; 99.8%; Pred. No. 1e-142; tive 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trans-sialidase; neuramidase; sleeping sickness;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone 121/151 encoding trans-sialidase gene active portion.
                                                                                                                                                                                                                         Sequence 500 BP; 119 A; 120 C; 147 G; 114 T; 0 U; 0 Other;
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                                                                                     Claim 23; Fig 22; 130pp; English.
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Chagas' Disease; parasite; ss
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                                                                                                                                                                                                                                                                     Best Local Similarity 99.8
Matches 499; Conservative
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P-PSDB; AAR42017
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                                                           infection.
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                                                                                                                                                                                            121 GATTITIGGCTGCTCTGAACCTGTGGCCCTTGAGTGGGAGGGGAAGCTCATCATAAACACC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T. cruzi complement regulatory protein; CRP; GPI anchor addition site; mammalian decay accelerating factor gene; DAF; plasmid pBC12B1-CRP/DAF; recombinant CRP eukaryotic expression cassette; Chagas' disease; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes modified Trypanosoma cruzi complement regulatory protein. The carboxy terminal end was modified to promote surface production in mammalian cells. The predicted GPI anchor addition site was removed and replaced with the C-terminal sequence of mammalian
                                                                                                      GAGGCTGTCGGCACGCTCTCACGTGTGGGGCCCCTCACCAAAATCGAACCAGCCCGGC
                                                                                                                            CGAGTTGACTATCGCCGCCGTCTGCAGTGTACAAGTCCAGTGACATGGGGAATTCGTGGGTG
                                                                     181 CGAGTTGACTGGAAACGCCCTCTGGTGTCGAGTCCAGTGACATGGAGAAACCGTGGGTG
                                                                                                                                                                        913 AGTCAGAGCAGCTTCACTGCCGTGACCATCGAGGGAATGCGTGTTATGCTCTTCACACAC
                                                                                                                                                                                                                                        CCGCTGAATTTTAAGGGAAGGTGGCTGCGCGACTGACCTCTGGCTGACGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          new vector encoding Trypanosoma cruzi complement regulatory protein, or treatment of Chaga's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/product= "Modified complement regulatory protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified T. cruzi CRP DNA with C-terminal mammalian DAF gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 25-29; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          GTCCTGTACAAGGATGATAA 1112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New trans-sialidase polypeptide(s) isolated from Trypanosoma - used for transferring sialic acid or for treating or preventing trypomastigote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clones 121 and 151, isolated from T.cruzi DNA library by homology to known neuramidase sequences, were found to have identical sequences in the region of the trans-sialidase gene necessary for enzymatic activity. The 121/151 nucleotide sequence (AAQ49559) is similar to the known TCNA sequence (AAQ49596) but distinct from the sequence of clone 154 (AAQ49597). N.B. the TCNA sequence shown in the SEQ.ID.Listing No.5 has the G nucleotide at position 486 missing. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                613 GCGTCCAACGGGAATCTTGTGTACCCTGTGCAGGTTACGAACAAAAAGAAGCAAGTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 673 TCCAAGATCTTCTACTCGGAAGACGAGGGCAAGACGTGGAAGTTTGGGGAGGTAGGAGT
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                                                                                                                                                                                                                                                              Trypanosome; trans-sialidase; neuramidase; sleeping sickness;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vandekerckhove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 500 BP; 124 A; 120 C; 147 G; 109 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .494
/*tag= a
/note= "has trans-sialidase activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.8%; Score 458.4; DB 2; 94.8%; Pred. No. 2.2e-130; ive 0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eichinger D,
                                                                                                                                                                                                                             TCNA trans-sialidase gene active portion.
GTCCTGTACAAGGATGATAA 1112
                    GTCCTGTACAAGGATGATAA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 22; Fig 22; 130pp; English.
                                                                                                              AAQ49596 standard; DNA; 500 BP.
                                                                                                                                                                                                                                                                                 Chagas' Disease; parasite; ss
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Matches 474; Conservative
                                                                                                                                                                                (revised)
(first entry)
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10-NOV-1992;
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26-APR-1994
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1093
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                                                                             RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding Trypanosoma cruzi complement regulatory protein, t of Chaga's disease.
                                                                CAACGGTATCACTTTGCAAACCACGCGTTCACGCTGGTGGCGTCGGTGACGATTCACGAG
                                                                                                                                                            Grecceracearrineceaaceachrinacricirereceacearerericarrase
                                                                                                                                                                                                          GTTCCG-----AGCGTCGCGAGTCCTTTGCTGGGTGCGAGCCTGGACTCTTCTGGT
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                                                                                                                                                                                                                                                                                                     GGCAAAAACTCCTGGGGCTCTCGTACGACGAGAAGCACCAGTGGCAGCCAATATACGGA
                          TTGAAGTTTGCGGGGGTTGGCGGAGGGGGCTTTTGGCCGGTGAGCCAGCAGCAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCAGTCGCTTGCCGCTGCCGCCGTTATGAGAATGTCGAATGGGA 1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T. cruzi complement regulatory protein; CRP; vac
Trypanosoma cruzi strain Y; Chagas' disease;
recombinant CRP eukaryotic expression cassette;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= b
/note= "GDS anchor addition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T. cruzi complement regulating protein DNA
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decay accelerating factor gene, which is recognised by mammalian cells. This was used in the construction of the plasmid pRCISBI-CRFDAF for production of recombinant CRF in mammalian cells. Recombinant CRF produced from host cells can be used as a vaccine to prime the immune system of an animal. Hybridomas secreting monoclonal antibodies recognising CRP are produced. This is used to detect Chagas's diseaserelated proteins and for treatment of the disease
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                                                                                                                                                                                                                             Score 186.6; DB 3; Length 3033;
Pred. No. 3.9e-46;
0; Mismatches 479; Indels 72;
                                                                                                                                                                                      Sequence 3033 BP; 786 A; 698 C; 897 G; 652 T; 0 U; 0 Other;
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Matches 636; Conservative
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                                                         GTTCCG------AGCGTCGCGAGTCCTTTGCTGGGTGCGAGCCTGGACTCTTCTGGT 1587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This novel DNA molecule was isolated by screening a Trypanosoma cruzi genomic expression library with pools of sera from infected individuals. It is the 5' end of an isolated clone; the 3' end is given in AAT69168. A full-length antigen (see AAW26541) is encoded by this sequence. 22 isolated DNA molecules (AAT69151-72) encode full-length antigens (see AAW16904-10, or epitope-containing repeats (see AAW18094-102, AAW19079-86 and AAW26542-44) of native antigens, that can be used in a variety of immunoassays for detecting T. cruzi infection in a blood, serum, plasma, saliva, cerebrospinal fluid or urine sample. The polypeptides are also useful in vaccines and pharmaceutical compositions for inducing saliva, cerebrospinal fluid or urine sample. The isolypeptides are also protective immunity against Chagas disease. The isolated DNA molecules can be used for recombinant production of the antigenic polypeptides. (Updated on 17-0CT-2003 to standardise OS field)
                                                                                       GCTCCGGAGACAGGCAGCCCCATCCCTTTGATGGGTGAGGGATGAACGATGCACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diagnosing Trypanosoma cruzi infection by detecting antibodies to novel antigens - which are useful in vaccines to provide protective immunity against Chagas' disease.
                                                                                                                       GGCAAAAAACTCCTGGGGCTCTCGTACGACGAGAAGCACCAGTGGCAGCCAATATACGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigen; epitope; vaccine; protective immunity; Chagas disease;
                                                                                                                                                                                  1648 TCAACGCCGGTGACGCCGACCGGATCGTGGGAGATGGGTAAGAGGTA 1694
                                                                                                                                                                                                                1987 GGCAGTĆGCTĠCĊĠĊŢĠCĊĠĠCGCATŤATĠAĠAATĠTCGAATĠĞĞA 2033
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Length 2446;
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Score 179; DB 2; L
Pred. No. 7.6e-44;
0; Mismatches 460;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The specification describes new Trypanosoma cruzi epitopes. A method for detecting Trypanosoma cruzi infection in a biological sample comprises contacting the sample with a polypeptide comprising an epitope of a TC antigen, or a variant of the antigen that differs only in conservative substitutions and/or modifications and detecting the presence of antibodies that bind to the polypeptide in the sample, thereby detecting antibodies that pind to the polypeptide in the sample, thereby detecting protection. The TC polypeptides can be used in vaccines for inducing protective immunity against Chagas' disease in a patient. The polypeptides and antibodies can also be used for detecting TC infection. AAX81740-61 represent nucleotides that encode TC epitopes from antigenic
                                                                                                                                               Trypanosoma cruzi epitope; Trypanosoma crużi infection; antigen; vaccine;
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Pred. No. 7.6e-44;
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DNA encoding recombinant FGF2 dimer.
          (first entry)
          23-JAN-2003
     ABV74081;
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Fibroblast growth factor 2; FGF2; human; dimerisation; vulnerary; cerebroprotective; cardiant; vasotropic; cytostatic; antlinflammatory; antiparkinsonian; nootropic; neuroprotective; gene; ss.

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/product= "FGF2 dimer"
                                          Location/Qualifiers
1. .1062
/*tag= a
Homo sapiens.
Synthetic.
Chimeric.
                                          Key
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WO200277199-A2

03-OCT-2002

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The present sequence is a coding sequence for a recombinant human (fibroblast growth factor 2 (FGF2) dimer. The encoded protein includes a fibroblast growth factor 2 (FGF2) dimer. The encoded protein includes a comprising 2 FGF monomers linked to one another and including at least come modification in an FGF monomer. The 2 monomers are preferably FGF2 monomers. Modifications include the replacement of a non-cysteine amino acid residues by a cysteine residue and the deletion of the 9 N-terminal and a read a residue by a cysteine residue and the deletion of the 9 N-terminal and a read are preferably FGF2 mino acid residues of at least one of the monomers. The resulting FGF dimer is used in claimed methods for promoting signal transduction, treating stroke, promoting angiogenesis, promoting sound healing, promoting collateral blood vessel formation, promoting nerve regenerating, preventing central or peripheral nervous system disease (e.g. Alzheimer's disease or Parkinson's disease). The FGF dimer can also be used to screen for compounds having FGF inhibitor activity. Such anglogenesis, treating chronic inflammation, and treating or preventing angiogenesis, treating chronic inflammation, and treating or preventing cancer, inhibiting anglogenesis, treating chronic inflammation, and treating or preventing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  composition of stabilized modified Fibroblast growth factor dimer, ful for promoting angiogenesis, nerve regeneration or wound healing, for treating or preventing stroke or other nervous disorders, and
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Pred. No. 9.6e-10;
0; Mismatches 2;
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                                                                                                   (MASI ) MASSACHUSETTS INST TECHNOLOGY
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                                                                                                                                                Shriver Z,
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                       27-MAR-2002; 2002WO-US009517.
                                                              27-MAR-2001; 2001US-0279165P.
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Job time : 1149 secs
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Sequence

Sequence

Sequence 1 Sequence 2 Sequence 2 Sequence 3 Sequence 3 Sequence 1 Sequence 2

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; Sequence 1, Application US/20030124109A1
; Publication No. US20030124109A1
; APPLICANT: Higuchi, Maria de Lourdes
; APPLICANT: Higuchi, Maria de Lourdes
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF
; TITLE OF INVENTION: MYCOFLASMA-ASSOCIATED DISEASES
; FILE REFERENCE: 33474-PCT-USA-A 068528.0103
; CURRENT APPLICATION NUMBER: PCT/BR01/00083
; PRIOR PLING DATE: 2002-03-01
; PRIOR PLING DATE: 2001-03-07
; PRIOR PLING DATE: 2001-03-07
; PRIOR FILING DATE: 2000-03-07
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 4
; SOFFWARE: FSELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Variant of T. Cruzi trans-sialidase gene
US-10-086-913-1
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                            US-10-417-923-6
US-10-417-923-6
US-10-267-311-11
US-09-876-348A-18
US-09-876-348A-36
US-09-876-348A-36
US-09-876-348A-36
US-09-876-348A-38
US-09-876-348A-38
US-09-876-796A-38
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US-10-231-298B-9
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100.0%; Pred. No. 0;
:ive 0; Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 2010; Conservative
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RESULT 1
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                                                                                                                August 8, 2004, 22:34:36; Search time 1262 Seconds (without alignments) 7809.280 Million cell updates/sec
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Sequence 1, Al
Sequence 33,
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Sequence 47,
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Sequence 60
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
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15: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-955-909-3
US-09-955-909-3
US-09-745-008-1
US-09-745-008-3
US-10-726-692-43
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US-10-423-156-69
US-10-108-195-5
US-10-204-070A-3
US-10-260-351-15
US-10-260-351-15
US-10-260-351-15
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                                                                                                                                                                                                                                                                                                        3222919 segs, 2451570024 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                    - nucleic search, using sw model
                                                                                                                                                                                                                                                    IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Gaps

61 ATGGCACCCGGATCGAGCCGAGTTGAGCTGTTTAAGCGGCAAAGCTCGAAGGTGCCATTT 120

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Sequence 5, A Sequence 3, A Sequence 15, Sequence 15, Sequence 15, Sequence 4, A

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Score

Result No.

1926.2 1886.6 1753.8 498.6 498.6 67.8 67.8 67.8 66.2 66.2

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                                                                                                                                                                                                                                                                               NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7188-032-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790990
TELEPHONE: (212)790900
           the Americas
                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,393
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 3183 base pairs
 STREET: 1155 Avenue of
                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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Matches 1931, Conserv
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Sequence 1, Application US/09745008 Patent No. US20020137667A1 GENERAL INFORMATION: APPLICANT: Chuenkova, Marina APPLICANT: Pereira, Miercio A.

RESULT 4 US-09-745-008-1

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GTTGCCATCGCGGACGCTCGCTACGAAACATCCAATGACAACTCCCTCATTGATACGGTG 258
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TITLE OF INVENTION: T. Cruzi-Derived Neurotrophic Agents and TITLE OF INVENTION: Methods of Use Therefor FILE REFERENCE: 1322.1028-001
CURRENT APPLICATION NUMBER: US/09/745,008
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 60/172,881
PRIOR FILING DATE: 1995-12-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                             Indels
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                                                                                                                                                                                             107;
                                                                                                                                                                       OB
                                                                                                                                                                       Score 1753.8;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                       87.3%;
                                                                                                                           ; TYPE: DNA
; ORGANISM: Trypanosoma cruzi
US-09-745-008-1
                                                                                                                                                                    Query Match
Best Local Similarity 94.3
Matches 1831, Conservative
                                                                                                                LENGTH: 2133
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Sequence No. US20020137667A1

GENERAL INFORMATION:

APPLICANT: Chuenkova, Marina

APPLICANT: Chuenkova, Miercio A.

ITLLE OF INVENTION: T. Cruzi-Derived Neurotrophic Agents and

ITLLE OF INVENTION: Methods of Use Therefor

FILE REFERENCE: 1322.1028-001

CURRENT APPLICATION NUMBER: US/09/745,008

CURRENT APPLICATION NUMBER: US 60/172,881

PRIOR FILING DATE: 1999-12-20

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 33

LENGTH 5403
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 93.3*;
Matches 1852; Conservative
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ORGANISM: Trypanosoma cruzi
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Db 1984 TTGGTTCTTACGATGACGAATAAATTGGCTCCGTGTACATTGATGAGAACTTCTGGAG 2043 1759 GGTTCAGGGCAGACCGTTGTCCCAGACGGACGACACTCCCACTTCTACGTT 1818	RESULT 6 US-10-726-692-43 i Sequence 43, Application US/10726692 ; Publication No. US20040132077A1 ; GENERAL INFORMATION: APPLICANT: KIRCHOFF, LOUIS V ; APPLICANT: KIRCHOFF, LOUIS V ; TITLE OF INVENTION: TRYPANOSOMA CRUZI ; TITLE OF INVENTION: TRYPANOSOMA CRUZI ; TITLE NEFERENCE: PIL21311A ; CURRENT APPLICATION NUMBER: US/10/726,692 ; CURRENT APPLICATION NUMBER: US 60/430,654 ; PRIOR FILING DATE: 2002-40-02	SEQ ID NO 43 SEQ ID NO 43 SEQ ID NO 43 SEQ ID NO 43	CAACCA GGGTTCACGGTGGTGGGTGGGTGATTCACG 15	
	979 AATTTTAAGGGAAGGTGGCTGCCGACCGACTCTGGCTGACGGATAACCAGCGC 1038	1219 ANTTGGGACAGCTACCAGCATTTGCACCCCTGGTGATCCAGCCGCTTGTCGTCA 1278	1399 GAGAGGGTCCGAACGGTTTGAAGTTTGCGGGGGGTTTGCGGGGGGTTTTG [684 GAGAGGGTTCGGAACGGTTTGAAGTTTGCGGGGGTTTGCGAAGGGGCGCTTTG [1459 AGCCACCAGGGGAGAATCACTTTGCAAACCACGGGTTTTGCGTTTGCAACCACGGTTTTGCAACCAGGGTTTTGCAACCAGGTTTTGCAAACCAGGGTTTCACTTTGCAAACCAGGGTTTCACGTTTTGCAAACCAGGGGTTCACGGTTTTGCAAACCAGGGGTTCAGGGGTTCAGGGGTTCGGTTTTGCAAACCAGGGGTTCAACGGGGTTCGAGGGGTTCGGGGGTTCGGGGGTTCGGGGGGGG	1804 1579 1864 1639 1699
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1895 TGAATGCCGAGGAGATCAGGACCTTGTTCTTGAGCCAGGACCTGATTGGCACGGAAGCAC 1954
                                    FEATURE:
OTHER INFORMATION: Synthetically generated oligonucleotide
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US-10-423-156-60
                                                                                            1955 ACATGGGCAGCAGCGGCAGCAGTGAAAGAAGTACGCC 1995
                                                                                                                                   482 ACATGGGCAGCAGCAGCAGTACCCCACGTACGCCC 522
                                                                                                                                                                                                                                                                                            APPLICANT: Lin, Hein-Yu
APPLICANT: Lin, Hein-Yu
APPLICANT: Hwong, Ching-Long
TITLE OF INVENTION: ANTIGENIC FRAGMENT OF HUMAN
TITLE OF INVENTION: T-LYMPHOTROPIC VIRUS
FILE REFERENCE: 05204-020001
CURRENT APPLICATION NUMBER: US,10/423,156
CURRENT FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: TW 91135980
FRIOR FILING DATE: 2002-12-12
NUMBER OF SEQ ID NOS: 60
SOFTWARE FRAEESEQ for Windows Version 4.0
SEQ ID NO 59
LENGTH: 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
3.5%; Score 69.4; DB 17;
Best Local Similarity 98.6%; Pred. No. 1.2e-11;
Matches 70; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-101.423-156-60
| Sequence 60, Application US/10423156
| Publication No. US20040116662A1
| GENERAL INFORMATION:
| APPLICANT: Lin, Hein-Yu
| APPLICANT: Lin, Hein-Yu
| APPLICANT: Lin, Hein-Yu
| TITLE OF INVENTION: ANTIGENIC FRAGMENT OF HUMAN
| TITLE OF INVENTION: ANTIGENIC FRAGMENT OF HUMAN
| TITLE OF INVENTION: T-LYMPHOTROPIC VIRUS
| FILE REPRESENCE: 65240-02001
| CURRENT FILING DATE: 2003-04-25
| PRIOR APPLICATION NUMBER: US/10/423,156
| PRIOR PLICATION NUMBER: W 91135980
| PRIOR PLING DATE: 2002-12-12
| NUMBER OF SEQ ID NOS: 60
| SEQ ID NO 60
| SEQ ID NO 60
| LENGTH: 759
                                                                                                                                                                                                                   US-10-423-156-59
's Sequence 59, Application US/10423156'
'Publication No. US20040116662A1
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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Sequence 47, Application US/10726692

Publication No. US20040132077A1

SEQUENCE 47, Application US/10726692

Publication No. US20040132077A1

APPLICANT: KIRCHHOFF, LOUIS V

APPLICANT: KIRCHHOFF, LOUIS V

TITLE OF INVENTION: TRYPANOSOMA CRUZI

TITLE OF INVENTION: TRYPANOSOMA CRUZI

FILE REFERENCE: PNL2311A

CURRENT APPLICATION NUMBER: US/10/726,692

CURRENT PILING DATE: 2003-12-04

PRIOR APPLICATION NUMBER: US 60/430,654

PRIOR PRIUNG DATE: 2002-04-02

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin version 3.2

LENGTH: 1557
                                                              GTGATATGCCAACCATAAGCCACGTGACGGTGAATAATGTTCTTTTACAACCGTCAGC 1894
                                                                                                                                              1895 TGAATGCCGAGGAGATCAGGACCTTGTTCTTGAGCCAGGACCTGATTGGCACGGAAGCAC 1954
                                                                                      362 GTGATATGCCAACCATAAGCCACGTGAAGGTGAATAATGTTCTTTACAACCGTCAGC 421
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1535 AGGTTCCGAGCGTCGCGAGTCCTTTGCTGGGTGCGAGCCTGGACTCTTCTGGTGGCAAAA 1594
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24.8%; Score 498.6; DB 17
Best Local Similarity 97.3%; Pred. No. 1.7e-153;
Matches 507; Conservative 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (1)..(1557)
US-10-726-692-47
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ORGANISM: T CRUZI
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                                  1 ATGGGCAGCCATCATCATCATCATCACAGCAGCGGCCTGGTGCCGCGGGGCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.3%; Score 66.2; DB 15; Length 72.3%; Pred. No. 1.1e-10; ive 0; Mismatches 33; Indels
                      4; Indels
Similarity 94.6%; Pred. No. 4.3e-11; 70; Conservative 0; Mismatches 4
                                                                                                                                                                                                                                                                        Publication No. US20030096753A1

REMERAL INFORMATION:
APPLICANT: University of Bristol
TITLE OF INVENTION: Therapeutic Agent
FILS REPERENCE: UNIBRISECT:
CURRENT PELLING DATE: 2002-10-01
FRIOR PILING DATE: 1988-04-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQUENCE: SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEUGTH: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
FILE PEPERSON
TITLE OF INVENTION: Therapeutic Agent
FILE PEPERSON
CURRENT APPLICATION NUMBER: US/10/260,352
CURRENT FILING DATE: 2002-10-01
PRIOR PELING DATE: 1988-04-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PETENTION VERSON 3.1
SERVING BATE: 1988-14-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: BETENTIN VERSON 3.1
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; Sequence 15. Application US/10260352
; Publication No. US20030097667A1
; GENERAL INFORMATION:
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Best Local Similarity 72.3%;
Matches 86; Conservative (
                                                                                                                                            61 ATGGCACCCGGATC 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
  Best Local Similarity
Matches 70; Conserv
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APPLICANT: Wan, Chi-Pong
APPLICANT: Venkataraman, Ganesh
APPLICANT: Shriver, Zachary
APPLICANT: Raman, Rahu,
APPLICANT: Sasisekharan, Ram
TITLE OF INVENTION: Methods and Products Related to FGF Dimerization
FILE REPERENCE: MOGES/10078 and Products Related to FGF Dimerization
CURRENT APPLICATION NUMBER: US/10/108,195
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10204070A; Sequence 3, Application US/10204070A; Publication No. US20040137588A1; General INFORMATION: APPLICANT: AMRAD Operations Pty Ltd; TITLE OF INVENTION: A method for producing recombinant molecules; FILE REFERENCE: 2379042/EJH; CURRENT APPLICATION NUMBER: US/10/204,070A; PRIOR APPLICATION NUMBER: US/10/204,070A; PRIOR PILING DATE: 2002-08-16; PRIOR PILING DATE: 2000-02-16; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3; LENGTH: 585
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Best Local Similarity 97.2%; Pred. No. 5e-11;
Matches 69; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Recombinant dFGF2 US-10-108-195-5
                                                                                                                                                                                                                                           Sequence 5, Application US/10108195; Publication No. US20030008820A1; GENERAL INFORMATION:
                                                                                                                                            424 ATGGCTTCCAGTAAAAGCC 442
                                                                                                         79
                                                                                                         61 ATGGCACCCGGATCGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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US-10-204-070A-3
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Publication No. US20030099664A1
GENERAL INFORMATION:
APPLICANT: Wishlewski, Jan
TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM
TITLE OF INVENTION: PUBLISERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS
TITLE OF INVENTION: PUBLISERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS
TITLE OF INVENTION: PUBLISERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS
CURRENT PILLUG DATE: 1050-10-11
PRIOR APPLICATION NUMBER: US/09/207,388
NUMBER OF SEQ ID NOS: 102
SOFTWARE: FEBLESEQ FOR WINDOWS VERSION 3.0
61 ATGCCACCCGGATCGAGCCGAGTTGAGCTGTTTAAGCGGCAAAGCTCGAAGGTGCCATT 119
                                                                           1 ATGGGCAGCAGCCATCATCATCATCACAGCAGCGGCCTGGTGCCGCGGGGCAGCCAT 60
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Fublication No. US20030219455A1
GENERAL INFORMATION:
APPLICANT: Cole, Garry T.
APPLICANT: Delgado, Nelson
APPLICANT: Yu, Jieh-Juen
APPLICANT: Yu, Jieh-Juen
APPLICANT: Xu, Jieh-Juen
APPLICANT: Xu, Jieh-Juen
APPLICANT: Xu, Jieh-Juen
TITLE OF INVENTION: USEFUL FOR IMMUNIZATION AGAINST COCCIDIOIDES SPP.
TITLE OF INVENTION: USEFUL FOR IMMUNIZATION AGAINST COCCIDIOIDES SPP.
TILE REFERENCE: 529522003300
CURRENT APPLICATION NUMBER: US 60/374,152
FRIOR PILING DATE: 2002-04-16
FRIOR FILING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 3
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3.2%; Score 65.2; DB 16; Length 1353;
Best Local Similarity 95.7%; Pred. No. 4.1e-10;
Matches 67; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
3.3%; Score 66; DB 15; Length 1989;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 66; Conservative 0; Mismatches 0; Indels
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; ORGANISM: Nesseria meningitidis
US-10-269-557-4
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LENGTH: 1989
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1 ATGGGCAGCCATCATCATCATCATCATCACAGCGGCCTGGTGCCGCGGGGCAGT 60

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2y 61 ATGCACCG 70

bb 61 ATGCCTACG 70

completed: August 9, 2004, 03:58
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Search completed: August 9, 2004, 03:58:53 Job time: 1265 secs

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Query Match
Best Local Similarity
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US-08-911-393-1
  Sequence 1, Applisequence 3, Applisequence 7, Applisequence 6, Applisequence 17, Applisequence 17, Applisequence 17, Applisequence 11, Applisequence 11, Applisequence 54, Applisequence 54, Applisequence 54, Applisequence 10, Applisequence 11, Applisequence 54, Applisequence 54, Applisequence 10, Applisequence 10, Applisequence 11, Applisequence 10, Applisequence 11, Applisequence 10, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applisequence 110, Applis
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Sequence 17,
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Sequence 54,
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(cgn2_6/ptodata/2/ina/5B_COMB.seq:*

(cgn2_6/ptodata/2/ina/6A_COMB.seq:*

(cgn2_6/ptodata/2/ina/6B_COMB.seq:*

(cgn2_6/ptodata/2/ina/ROTUS_COMB.seq:*

(cgn2_6/ptodata/2/ina/ROTUS_COMB.seq:*

(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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PCT-US93-02869-7
PCT-US93-02869-6
PCT-US93-02869-6
US-08-993-674A-17
US-09-256-976-17
US-09-213-303-11
US-09-213-303-11
US-09-237-308-4
US-09-237-308-4
US-09-237-308-11
US-09-267-311-54
US-09-267-311-54
US-09-267-311-54
US-09-267-311-54
US-09-267-311-54
US-09-198-723A-111
US-09-684-881-111
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US-09-198-723A-112
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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US-09-684-881-112
US-09-684-881-113
US-09-684-881-114
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US-09-198-723A-92
US-09-198-723A-94
US-09-198-723A-96
US-09-198-723A-96
US-09-198-723A-96
US-09-198-723A-99
US-09-198-723A-100
US-09-198-723A-101
US-09-198-723A-101
US-09-198-723A-101
US-09-684-881-92
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US-09-684-881-93
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10036-271
COMPUTER READABLE FORM:
MEDIUM TYER: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTESEQ VOTSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,393
FILING DATE: 14-AUG-1997
CLASSIPICATION HATA:
APPLICATION NUMBER: 30,742
FILING DATE: ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A
REGISTRATION NUMBER: 30,742
RETERENCE/DOCKET NUMBER: 7188-032-9:
TELECOMMUNICATION INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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      AATTTTTCCCGGCGGAAATGGAAGGAATGCACACAAATCAATTTCTTGGCGGTGCAGGTG
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Pred. No. 0;
0; Mismatches
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: PERNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
CITY: New York
COUNTRY: UGA
ZIP: 10036-2711
COMPUTER: READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast SEQ, Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,393
FILING DATE: 14-AUG-1997
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WEILING DATE:
APPLICATION NUMBER: US/08/911,393
FILING DATE: TANDORDATION
                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: COCALZI, LAULA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7188-032-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)799990
TELEPHONE: (212)799990
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1929 base pairs
TYPE: nucleic acid
STRANDENESS:
TOPOLOGY: linear
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Best Local Similarity 98.8%;
Matches 1901; Conservative
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GENERAL INFORMATION:
APPLICANT: NUSSENZWEIG, VICTOR
APPLICANT: SCHENKAAN, SERGIO
APPLICANT: VAN DEN KERKOV, PHILIP
APPLICANT: BICHINGER, Daniel
TITLE OF INVENTION: TRANS-STALIDASE AND METHODS OF USE
TITLE OF INVENTION: TRANS-STALIDASE AND METHODS OF USE
TITLE OF INVENTION: TRANS-STALIDASE AND
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: Z0004
                                                                                                                                                                       Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02869
FILING DATE: 19930325
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/07/857,519
FILING DATE: 24-MAR-1992
                                                                                                Score 498.4; DB 5;
Pred. No. 4.6e-145;
0; Mismatches 1;
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                                                                                                    24.8%;
                                                                                                                                                                Matches 499; Conservative
                                                                                         Query Match
Best Local Similarity
                          PCT-US93-02869-3
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1805 CGGTGAATAATGTTCTTTACAACCGTCAGCTGAATGCCGAGGAGATCAGGACCTTGT 1864
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PCT-US93-02869-3
FCT-US93-02869-3
FGENERAL INFORMATION:
APPLICANT: WASRIXWEIG, VICTOR
APPLICANT: SCHENMAN, SERGIO
APPLICANT: BICHINGER, Daniel
TITLE OF INVENTION: TRANS-SIALIDASE AND METHODS OF USE
TITLE OF INVENTION: TRANS-SIALIDASE AND METHODS OF USE
TITLE OF INVENTION: TRANS-SIALIDASE AND METHODS OF USE
TITLE OF INVENTION: ADDRESS:
ADDRESSE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STREET: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER: READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: BLORDY disk
COMPUTER: BLORDY disk
COMPUTER: Patentin Release #1.0, Version #1.25
GOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US93/02869
FILING DATE: 24-MAR-1992
ATTORNEY ASPLICATION DATA:
APPLICATION NUMBER: US/O7/857,519
FILING DATE: 24-MAR-1992
ATTORNEY AGENT INFORMATION:
NAME: TOWNSEND, GUY KENT.
NAME: TOWNSEND, GUY KENT.
NAME: TOWNSEND, GUY KENT.
TELECHOMMUTCATION INPORMATION:
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TYPE: NUCLEIC ACID
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 500 base pairs
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CCGCTGAATTTTAAGGGAAGGTGGCTGCGCGACCGACTGAACCTCTGGCTGACGGATAAC 1032
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                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02869
FILING DATE: 19930325
                                                                                                                                                                                                      FILING DATE: 15730325
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/857,519
FILING DATE: 24-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNESND, GUY KEVIN
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: NUSSENZWEIG 1A
TELEPHONE: 202-628-5197
TELEPHONE: 202-737-3528
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TYPE: NUCLEIC ACID
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
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                                      ZIP: 20004
COMPUTER READABLE FORM:
D.C.
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GENERAL INFORMATION:
APPLICANT: NUSSENTWEIG, VICTOR
APPLICANT: SCHENKMAN, SERGIO
APPLICANT: EICHINGER, Daniel
TITLE OF INVENTION: TRANS-SIALIDASE AND METHODS (
TITLE OF INVENTION: TRANS-SIALIDASE AND METHODS (
TITLE OF INVENTION: AND MAKING THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                 Score 498.4; DB 5;
Pred. No. 4.6e-145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHODS
              NAME: TOWNSEND, GUY KEVIN
REGISTRATION NUMBER: 34,033
REPERENCE/DOCKET NUMBER: NUSSENZWEIG 1A
TELEPHONE: 202-628-5197
TELEPHONE: 202-37-3528
TELERA: 202-37-3528
TELERA: 202-37-3528
TELERA: 248633
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
TYPE: NUCLEIC ACID
STRANDENNES: single
                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                               Query Match 24.8%;
Best Local Similarity 99.8%;
Matches 499; Conservative
    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                             PCT-US93-02869-7
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1033 CAGCGCATTTATAACGTTGGGCAAGTATCCATTGGTGAAAATTCCGCCTACAGCTCC 1092
301 AGTCAGACGAGCTTCACTGCCGTGACCATCGAAGGAATGCGTGTGATGCTCTTCACACAC 360
                                                                                                                                                                                                                                           647 TTACGAACAAAAGGAAGTTTTTCCAAGATCTTCTACTCGGAAGACGAGGCCAAGA 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/08834306
| Patent No. 6054135
| Patent No. 6054135
| Patent No. 6054135
| Patent No. 6054135
| Patent No. 6054135
| Patent No. 6054135
| Papricant: Lodes, Michael J. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Houghton, Raymond L. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PRINTING OF SEQUENCES: 65
| CORRESPONDENCE ADDRESS: 65
| CORRESPONDENCE ADDRESS: 65
| CORRESPONDENCE SEED and BERRY LLP | STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle | STREET: Washington COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY. HOLD | COLUMNEY.
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8.9%; Score 179; DB 3; Length 2446;
Best Local Similarity 51.3%; Pred. No. 3.9e-45;
Matches 494; Conservative 0; Mismatches 460; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UGA

ZIP: 98104-7092

ZIP: 98104-7092

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,306
FILING DATE: 15-APR-1997
                                                                                                                                                                                                                                                                                                                                               GTCCTGTACAAGGATGATAA 1112
                                                                                                                                                                                                                                                                                                                                                                                   TLLING DALE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MARK, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21012
TELECHMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-601
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2446 base pairs
TYPE: NUCleic acid
STRANDENESS: single
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US-08-834-306-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     733 GATTITGGCIGCICTGAACCIGTGGCCCTIGAGIGGGAAGGICATCAIAAACACI 792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 GAGGCTGTCGCGAGCCTCTCGCGTGTGTGGGGCCCCTCACCAAAATCGAACCAGCCCGGC 300
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                         Sequence 5, Application PC/TUS9302869
Sequence 5, Application PC/TUS9302869
GENERAL INFORMATION:
APPLICANT: NUSSENZWEIG, VICTOR
APPLICANT: SCHENGAN, SERGIO
APPLICANT: WAN DEN KERKOV, PHILIP
APPLICANT: BICHINGER, Daniel
TITLE OF INVENTION: TRANS-SIALIDASE AND METHODS OF USE
TITLE OF INVENTION: TRANS-SIALIDASE AND
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: INPO GOMPATIBLE
COMPUTER: THE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02869
FILING DATE: 19930325
CLASSIFFCATION:
PRICATION NUMBER: US/07/857,519
FILING DATE: 24-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, GUT KEVIN
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 34,033
                                                                                                                                                                                                                                                                                                                                                                                       E: Browdy and Neimark
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
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PCT-US93-02869-5
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TELEX: 248633
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 499 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 419 Sevent CITY: Washington STATE: D.C.
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Best Local Similarity
Matches 473; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.9%; Score 179; DB 3; Length 2446;
51.3%; Pred. No. 3.9e-45;
Ive 0; Mismatches 460; Indels
                                                                                                                                                       #1.30
                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,674A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                   210121.422C2
                                                                                                       COMPUTER: IBM PC COMPALATION OPERATING SYSTEM: PC-DOS/MS-DOS COPTWARE: Patentin Release #1.0,
                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                   ; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 17
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2446 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
;; TOPOLOGY: linear
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Conservative
                  Washington
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                                                        98104-7092
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                                       COUNTRY:
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APPLICANT: Reed, Steven G.
APPLICANT: Skeik, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Moughton, Raymond L.
APPLICANT: Smith, John M.
APPLICANT: Moust, John M.
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APPLICANT: Smith, John M.
APPLICANT: Moust, John M.
APPLICANT: SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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Patent No. 6497880

GENERAL INCORMATION:
TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM
TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM
TITLE OF INVENTION: PUMICATUS
TITLE OF INVENTION: PUMICATUS
TITLE OF INVENTION: PUMICATUS
TITLE OF INVENTION: 1090-121
CURRENT APPLICATION NUMBER: US/09/207,388
CURRENT APPLICATION NUMBER: US/09/207,388
CURRENT PILING DATE: 1996-12-08
NUMBER OF SEQ ID NOS: 102
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
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; TYPE: DNA
; ORGANISM: Nesseria meningitidis
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GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodge, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Morelll, Particial D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION
TITLE OF INVENTION: OF T. CRUZI INFECTION
TITLE OF INVENTION: OF T. CRUZI INFECTION
TITLE OF INVENTION: OF T. CRUZI INFECTION
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TITLE OF INVENTION: OF T. CRUZI INFECTION
TITLE OF INVENTION WORBER: US/09/256, 976
CURRENT FILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 95
SEC ID NO 17
1480
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llarity 51.3%; Pred. No. 3.9e-45;
Conservative 0; Mismatches 460; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Trypanosoma cruzi
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Best Local Similarity
Matches 494; Conserv
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US-09-256-976-17
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Sequence 3, Application US/09230078A

Sequence 3, Application US/09230078A

Patent No. 6495334

GENERAL INPORMATION:
APPLICANT: Rajashekara, Gireesh
APPLICANT: Rajushekara, Gireesh
APPLICANT: Rajushekara, Gireesh
APPLICANT: Rapur, Vivek
TILE REFERENCE: 600.335USWO
CURRENT APPLICATION NUMBER: US/09/230,078A

CURRENT APPLICATION NUMBER: CT/US97/12639
PRIOR APPLICATION NUMBER: ECT/US97/12639
PRIOR APPLICATION NUMBER: 60/022,191
PRIOR APPLICATION NUMBER: 60/022,191
PRIOR APPLICATION NUMBER: 60/022,191
PRIOR APPLICATION NUMBER: 60/022,191
PRIOR PLING DATE: 1996-07-19

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3

LENGTH: 552
                                                                                                                                                                                                                                                                                                              Sequence 54, Application US/09613303
Patent No. 6495347
Batent INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REPERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/09/613,303
                                                                                                                                                                                           Query Match 3.2%; Score 65; DB 4; Length 366; Best Local Similarity 100.0%; Pred. No. 3.9e-10; Matches 65; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 5.1e-10;
.ive 0; Mismatches 0; Indels
                                                                 OTHER INFORMATION: fusion sequence
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Matches 65; Conservative
                                                                                     ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(363)
US-10-267-311-11
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US-09-230-078A-3
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APPLICANT: Mizzen, Lee A.
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/00201
CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR PRILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 366
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APPLICANT: Chu, N. Randall
APPLICANT: Chu, N. Randall
APPLICANT: M. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR PILING DATE: 12000-07-10
PRIOR PILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PASLSEQ for Windows Version 4.0
                        Length 1989;
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                                                                 Indels
         3.3%; bcc.
100.0%; Pred. No. ____
0; Mismatches
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3.2%; Score 65; DB
Best Local Similarity 100.0%; Pred. No. 3.9
Matches 65; Conservative 0; Mismatches
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Patent No. 6495347
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NAME/KEY: CDS
OCATION: (1)...(363)
US-613-303-11
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Patent No. 6657055
GENERAL INFORMATION:
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               Query Match
Best Local Similarity 100.
Marches 66; Conservative
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LENGTH: 366
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i Sequence 54, Application US/10267311

i Patent No. 6657055

i GENERAL INFORMATION:

APPLICANT: Siegel, Marvin

APPLICANT: Mizzen, Lee A.

ITILE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO

FILE REFERENCE: 12071/002001

CURRENT FILING DATE: 2002-10-09

PRIOR FILING DATE: 2002-10-09

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 1999-07-08

NUMBER OF SEQ ID NOS: 55

SOUTHARD: FLIENG DATE: 1000-07-10

PRIOR FILING DATE: 1000-07-10

PRIOR FILING DATE: 2000-07-10

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CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: RestSEQ for Windows Version 4.0
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Job time : 173 secs
                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
NAME/KEY: CDS
LOCATION: (1)...(1227)
US-09-613-303-54
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ORGANISM: Artificial Sequence
FBATURE:
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; NAME/KEY: CDS
; LOCATION: (1)...(1227)
US-10-267-311-54
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LENGTH: 1230
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